

FIGURE 1

CAGCGCGTGGCCGGCGCCGCTGTGGGGACAGCATGAGCGGCGGTTGGATGGCGCAGGTTGGAGCGTGGCGAACA
GGGGCTCTGGGCCTGGCGCTGCTGCTGCTGCTCGGCCTCGGACTAGGCCTGGAGGCCGCCGCGAGCCCGCTTTC
CACCCCGACCTCTGCCCAGGCCGCAGGCCCCAGCTCAGGCTCGTGCCACCCACCAAGTTCCAGTGCCGCACCA
GTGGCTTATGCGTGCCCCCTCACCTGGCGCTGCGACAGGGACTTGGACTGCAGCGATGGCAGCGATGAGGAGGAG
TGCAGGATTGAGCCATGTACCCAGAAAAGGGCAATGCCACCGCCCCCTGGCCTCCCCCTGCCCTGCACCGGCGT
CAGTGACTGCTCTGGGGGAAC TGACAAGAACTGCGCAACTGCAGCCGCCTGGCCTGCCTAGCAGGCGAGCTCC
GTTGCACGCTGAGCGATGACTGCATTCCACTCACGTGGCGCTGCGACGGCCACCCAGACTGTCCCGACTCCAGC
GACGAGCTCGGCTGTGGAACCAATGAGATCCTCCCGGAAGGGGATGCCACAACCATGGGGCCCCCTGTGACCCT
GGAGAGTGTACCTCTCTCAGGAATGCCACAACCATGGGGCCCCCTGTGACCCTGGAGAGTGTCCCTCTGTGCG
GGAATGCCACATCCTCCTCTGCCGGAGACCAGTCTGGAAGCCCAACTGCCTATGGGGTTATTGCAGCTGCTGCG
GTGCTCAGTGCAAGCCTGGTCACCGCCACCCCTCCTCCTTTTGTCTGGCTCCGAGCCCAGGAGCGCCTCCGCCC
ACTGGGGTTACTGGTGGCCATGAAGGAGTCCCTGCTGCTGTCA~~GA~~AACAGAAGACCTCGCTGCCCTGAGGACAAG
CACTTGCCACCACCGTCACTCAGCCCTGGGCGTAGCCGGACAGGAGGAGAGCAGTGATGCGGATGGGTACCCGG
GCACACCAGCCCTCAGAGACCTGAGTTCTTCTGGCCACGTGGAACCTCGAACCCGAGCTCCTGCAGAAGTGGCC
CTGGAGATTGAGGGTCCCTGGACACTCCCTATGGAGATCCGGGGAGCTAGGATGGGGAACCTGCCACAGCCAGA
ACTGAGGGGCTGGCCCCAGGCAGCTCCCAGGGGGTAGAACGGCCCTGTGCTTAAGACACTCCCTGCTGCCCCGT
CTGAGGGTGGCGATTAAAGTTGCTTC

FIGURE 2

MSGGWMAQVGAWRGTGALGLALLLLLGLGLGLEAAASPLSTPTSAQAAGPSSGSCPPTKFCQRTSGLCVPLTWRC
DRDLDCSDGSDDEEECRIEPCCTQKGQCPCPPPGLPCTGVSDCSGGTDKKLRNCSRLACLAGELRCTLSDDCIPL
TWRCDGHPDCPDSSDELGCGTNEILPEGDATTMGPPVTLESVTSLRNATTMGPPVTLESVPSVGNATSSSAGDQ
SGSPTAYGVIAAAAVLSASLVTATLLLLLSWLRAQERLRPLGLLVAMKESLLLSEQKTSLP

Signal sequence:

amino acids 1-30

Transmembrane domain:

amino acids 230-246

N-glycosylation site.

amino acids 126-130, 195-199, 213-217

Casein kinase II phosphorylation site.

amino acids 84-88, 140-144, 161-165, 218-222

N-myristoylation site.

amino acids 3-9, 10-16, 26-32, 30-36, 112-118, 166-172, 212-218, 224-230,
230-236, 263-269

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 44-55

Leucine zipper pattern.

amino acids 17-39

FIGURE 3

ACACTGGCCAAACACTCGCATCCCAGGGCGTCTCCGGCTGCTCCCATTTGAGCTGTCTGCT
CGCTGTGCCCCGCTGTGCCTGCTGTGCCCCGCGCTGTCGCCGCTGCTACCGCGTCTGCTGGA
CGCGGGAGACGCCAGCGAGCTGGTGATTGGAGCCCTGCGGAGAGCTCAAGCGCCCAGCTC
TGCCCGAGGAGCCCAGGCTGCCCCGTGAGTCCCATAGTTGCTGCAGGAGTGGAGCCTTTC
CCTTTGCGATCGCTAAACCACCATGAGCTGCGTCTCTGGGTGGTGTTCATCCCCCTTGGGGCT
GCTGTTCCCTGGTCTGCGGATCCCAAGGCTACCTCCTGCCCAACGTCACTCTCTTAGAGGA
GCTGCTCAGCAAATACCAGCACAAACGAGTCTCACTCCCGGGTCCGCAGAGCCATCCCCAG
GGAGGACAAGGAGGAGATCCTCATGCTGCACAACAAGCTTCGGGGCCAGGTGCAGCCTCA
GGCCTCCAACATGGAGTACATGACCTGGGATGACGAACTGGAGAAGTCTGCTGCAGCGTG
GGCCAGTCAGTGCATCTGGGAGCACGGGCCACCAGTCTGCTGGTGTCCATCGGGCAGAA
CCTGGGCGCTCACTGGGGCAGGTATCGCTCTCCGGGGTTCCATGTGCAGTCCTGGTATGA
CGAGGTGAAGGACTACACCTACCCCTACCCGAGCGAGTGCAACCCCTGGTGTCCAGAGAG
GTGCTCGGGGCCTATGTGCACGCACTACACACAGATAGTTTGGGGCCACCACCAACAAGAT
CGGTTGTGCTGTGAACACCTGCCGGAAGATGACTGTCTGGGGAGAAGTTTGGGAGAACGC
GGTCTACTTTGTCTGCAATTATTCTCCAAAGGGGAAC'TGGATTGGAGAAGCCCCCTACAA
GAATGGCCGGCCCTGCTCTGAGTGCCCAACCAGCTATGGAGGCAGCTGCAGGAACAAC'TT
GTGTTACCGAGAAGAAACCTACACTCCAAAACCTGAAACGGACGAGATGAATGAGGTGGA
AACGGCTCCCATTCCTGAAGAAAACCATGTTTGGCTCCAACCGAGGGTGATGAGACCCAC
CAAGCCCAAGAAAACCTCTGCGGTCAACTACATGACCCAAGTCGTCAGATGTGACACCAA
GATGAAGGACAGGTGCAAAGGGTCCACGTGTAACAGGTACCAGTGCCCAGCAGGCTGCCT
GAACCACAAGGCGAAGATCTTTGGAAGTCTGTTCTATGAAAGCTCGTCTAGCATATGCCG
CGCCGCCATCCACTACGGGATCCTGGATGACAAGGGAGGCC'TGGTGGATATCACCAGGAA
CGGGAAGTCCCCCTTCTTCGTGAAGTCTGAGAGACACGGCGTGCAGTCCCTCAGCAAATA
CAAACCTTCCAGCTCATTTCATGGTGTCAAAAGTGAAAGTGCAGGATTTGGACTGCTACAC
GACCGTTGCTCAGCTGTGCCCGTTTGAAAAGCCAGCAACTCACTGCCCAAGAATCCATTG
TCCGGCACACTGCAAAGACGAACCTTCCTACTGGGCTCCGGTGT'TTGGAACCAACATCTA
TGCAGATACCTCAAGCATCTGCAAGACAGCTGTGCACGCGGGAGTCATCAGCAACGAGAG
TGGGGGTGACGTGGACGTGATGCCCCGTGGATAAAAAAGAAGACCTACGTGGGCTCGCTCAG
GAATGGAGTTCAGTCTGAAAGCCTGGGGACTCCTCGGGATGGAAGGCCTTCCGGATCTT
TGCTGTCAGGCATTTCCCTTTGCGGCCGCGTGAATTTCCAGCACCAGGGGAGAAGGGGCG
TCTTCAGGAGGGCTTCGGGGTTTTGCTTTTATTTTATTTTGTATTGCGGGGTATATGG
AGAGTCA

FIGURE 4

MSCVLGGVPLGLLFLVCGSQGYLLPNVTLLLELLSKYQHNEHSRVRRRAIPREDKEEIL
 MLHNKLRGQVQPQASNMEYMTWDDELEKSAAAWASQCIWEHGPTSLLVSIGQNLGAHWGR
 YRSPGFHVQSWYDEVKDYTYYPSECNPWCPCRCGPMCTHYTQIVWATTNKIGCAVNTC
 RKMTVWGEVWENAVYFVCNYSKGNWIGEAPYKNGRPCSECPPSYGGSCRNNLCYREETY
 TPKPETDEMNEVETAPIPEENHVWLQPRVMRPTKPKKTSAVNYMTQVVRCDTKMKDRCKG
 STCNRYQCPAGCLNHKAKIFGSLFYESSSSICRAAIHYGILDDKGGLVDITRNGKVPFFV
 KSERHGVQSLSKYKPSSSFMVSKVKVQDLDCYTTVAQLCPFEEKPATHCPRIHCPAHCKDE
 PSYWAPVFGTNIYADTSSICKTAVHAGVISNESGGDVDMPVDKKKTYVGSLRNGVQSES
 LGTPRDGKAFRIFAVRQ

Important features of the protein:Signal peptide:

1-22

N-glycosylation site:

27-31

41-45

451-455

cAMP- and cGMP-dependent protein kinase phosphorylation site.

181-185

276-280

464-468

Tyrosine kinase phosphorylation site.

385-393

N-myristoylation site.

111-117

115-121

174-180

204-210

227-233

300-306

447-453

470-476

Extracellular proteins SCP/Tpx-1/Aq5/PR-1/Sc7 signature 2.

195-207

SCP-like extracellular protein

56-208

FIGURE 5

CTGTCAGGAAGGACCATCTGAAGGCTGCAATTTGTTCTTAGGGAGGCAGGTGCTGGCCTGGCCTGGATCTTCCA
CCATGTTTCCTGTTGCTGCCTTTTGATAGCCTGATTGTCAACCTTCTGGGCATCTCCCTGACTGTCCTCTTCACC
CTCCTTCTCGTTTTTCATCATAGTGCCAGCCATTTTTGGAGTCTCCTTTGGTATCCGCAAACCTCTACATGAAAAAG
TCTGTTAAAAATCTTTGCGTGGGCTACCTTGAGAATGGAGCGAGGAGCCAAGGAGAAGAACACCAGCTTTACA
AGCCCTACACCAACGGAATCATTGCAAAGGATCCCACTTCACTAGAAGAAGAGATCAAAGAGATTTCGTGGAAGT
GGTAGTAGTAAGGCTCTGGACAACACTCCAGAGTTCGAGCTCTCTGACATTTTCTACTTTTGCCGAAAGGAAT
GGAGACCATTATGGATGATGAGGTGACAAAGAGATTCTCAGCAGAAGAACTGGAGTCTTGGAACTGCTGAGCA
GAACCAATTATAACTTCCAGTACATCAGCCTTCGGCTCACGGTCTGTGGGGGTTAGGAGTGTGATTTCGGTAC
TGCTTTCTGCTGCCGCTCAGGATAGCACTGGCTTTACAGGGATTAGCCTTCTGGTGGTGGGCACAACCTGTGGT
GGGATACTTGCCAAATGGGAGGTTTAAGGAATTCATGAGTAAACATGTTTCACTTAATGTGTTACCGGATCTGCG
TGCGAGCGCTGACAGCCATCATCACCTACCATGACAGGGAAAACAGACCAAGAAATGGTGGCATCTGTGTGGCC
AATCATACCTCACCGATCGATGTGATCATCTTGGCCAGCGATGGCTATTATGCCATGGTGGGTCAAGTGCACGG
GGGACTCATGGGTGTGATTTCAGAGAGCCATGGTGAAGGCCTGCCACACGTCCTGGTTTGAGCGCTCGGAAGTGA
AGGATCGCCACCTGGTGGCTAAGAGACTGACTGAACATGTGCAAGATAAAAGCAAGCTGCCTATCCTCATCTTC
CCAGAAGGAACCTGCATCAATAATACATCGGTGATGATGTTCAAAAAGGGAAGTTTTGAAATTGGAGCCACAGT
TTACCCCTGTTGCTATCAAGTATGACCCCTCAATTTGGCGATGCCTTCTGGAACAGCAGCAAATACGGGATGGTGA
CGTACCTGCTGCGAATGATGACCAGCTGGGCCATTGTCTGCAGCGTGTGGTACCTGCCTCCCATGACTAGAGAG
GCAGATGAAGATGCTGTCCAGTTTGCGAATAGGGTGAAATCTGCCATTGCCAGGCAGGGAGGACTTGTGGACCT
GCTGTGGGATGGGGGCTGAAGAGGGGAGAAGGTGAAGGACACGTTCAAGGAGGAGCAGCAGAAGCTGTACAGCA
AGATGATCGTGGGGAACCAAGGACAGGAGCCGCTCCTAGCCCTGCCTCCAGCTGGCTGGGGCCACCGTGCGG
GGTGCCAACGGGCTCAGAGCTGGAGTTGCCGCCGCCGCCCCCACTGCTGTGTCTTTCCAGACTCCAGGGCTCC
CCGGGCTGCTCTGGATCCCAGGACTCCGGCTTTTCGCCGAGCCGACGCGGGATCCCTGTGCACCCGGCGCAGCCT
ACCTTTGGTGGTCTAAACGGATGCTGCTGGGTGTTGCGACCCAGGACGAGATGCCTTGTTTTCTTTTACAATAAG
TCGTTGGAGGAATGCCATTAAAGTGAACCTCCCCACCTTTGCACGCTGTGCGGGCTGAGTGGTTGGGGAGATGTG
GCCATGGTCTTGTGCTAGAGATGGCGGTACAAGAGTCTGTTATGCAAGCCGTGTGCCAGGGATGTGCTGGGGG
CGGCCACCCGCTCTCCAGGAAAGGCACAGCTGAGGCACTGTGGCTGGCTTCGGCCTCAACATCGCCCCCAGCCT
TGGAGCTCTGCAGACATGATAGGAAGGAACTGTCATCTGCAGGGGCTTTTCAAGAAAATGAAGGGTTAGATTTT
TATGCTGCTGCTGATGGGGTTACTAAAAGGAGGGGAAGAGGCCAGGTGGGCCGCTGACTGGGCCATGGGGAGAA
CGTGTGTTTCGTACTCCAGGCTAACCTGAACCTCCCATGTGATGCGCGCTTTGTTGAATGTGTGTCTCGGTTC
CCCATCTGTAATATGAGTCGGGGGGAATGGTGGTGAATTCCTACCTCACAGGGCTGTTGTGGGGATTAAAGTGCT
GCGGGTGAGTGAAGGACACATCACGTTCAGTGTTTCAAGTACAGGCCCACAAAACGGGGCACGGCAGGCCTGAG
CTCAGAGCTGCTGCACTGGGCTTTGGATTTGTTCTTGTGAGTAAATAAAAAGCTGGCTGGTGAATGA

FIGURE 6

MFLLLPFD SLIVNLLGISLTVLFTLLLVFIIVPAIFGV SFGIRKLYMKSLLKIFAWATLRMERGAKEKNHQLYK
PYTNGIIAKDPTSLEEEIKEIRRS GSSKALDNTPEFELSDIFYFCRKGMETIMDDEVTKRFSAEELSWNLLSR
TNYNFQYISLRLTVLWGLGV LIRYCFLPLRIAL AFTGISLLVVGTTVVGYPNGRFKEFMSKHVHLMCYRICV
RALTAIITYHDRENRP RNGGICVANHTSPIDV IILASDGYAMVGQVHGGLMGVIQ RAMVKACPHVWFERSEVK
DRHLVAKRLTEHVQDKSKLPILIFPEGTCINNTSVM MFKKGSFEIGATVYPVAIKYDPQFGDAFWNSSKYGMVT
YLLRMMTSWAIVCSVWYLP PMTREADED AVQFANRVKSAIARQGGLVDLLWDGGLKREKVKDTFKEEQQKLYSK
MIVGNHKDRSRS

FIGURE 7A

CTCCCTTTCATCTGGTGGCCCTAGCGCCACAAGCTGCCGCTTAGGAAGTCCCTGCCGGGA
GCAGAAAGTGGAGACATCAGCAGGATGGCATCGGCAAGTCGCTCCCTCCCGGGCCTCATC
TGCCAAACGATCATCTCCTCCTCCGAAGTTGTATGCATGACAGGCGAGTGAAAACCTTCAC
TAAAAATGAAGGCGATTGACACAACAGAAGGAACTCCATCCTTTCGGGGGCTTACGAAAAT
AATAAGTTTAAAAAAAATAGGAAGGGAATTCCCTCGCTCCATGATCACTGAGCGCTCTCC
TAAGGAAAAGGAAATCTCCCGGGGGGTGCCGACTACGGGCGGCGGGCTTAGGATGCTCCC
ACGCTCCCCGACCCCAATCCCCAGGACCCGACGACCTCCGGAGGAACGCCCCGCCAGCC
CGCCCGGAGCCACGCGGCACAAGGTGACACGGACCGCGCCGCGCGGGCCCCCTCAGCCGCC
TGGGCGAGGCCGGGAGCAGGGAGAGGGGCATCCGCCGGCCCGCGGTACCTTGTAATTATC
AAAGCCAGCCAGCTGCTCCGGGCTCACGTATTCTGTAGCCAGCCATGACGACCCGAAAACCT
GAGCGCCCACTCGGCAGCGACTCCCGGCTACAAGGCTGTGACACACAAGCACCACACCGG
CTGGGCAAGGATGGCAAAGACTGGGCTGCCCCGAGAAGGGACAGAGTCAGGCTGGAGGGGA
ATCTGGATCTGGGCAGCTCCTGGACCAAGAGAATGGAGCAGGGGAATCAGCGCTGGTCTC
CGTCTATGTACATCTGGACTTTCCAGATAAGACCTGGCCCCCTGAACTCTCCAGGACACT
GACTCTCCCTGCTGCCTCAGCTTCTCTTCCCCAAGGCCTCTTCTCACTGGCCTCAGACT
CACAAACAGGTGAGTACATGAGCTGCTTCGAGGCCCAGGGCTTCAAGTGGAACCTGTATGA
GGTGGTGAGGGTGCCCTTGAAGGCGACAGATGTGGCTCGACTTCATACCAGCTGTCCAT
CTCCTGTGTACCTCCCCTGGCTTCCAGCTGAGCTGCTGCATCCCCAGCACAAACCTGGC
CTACACCGCGGCCTGGAGCCCTGGAGAGGGCAGCAAAGCTTCCTCCTTCAACGAGTCAGG
CTCTCAGTGCTTTGTGTCTGGCTGTTTCAGCGCTGCCCGATGGCTGACACCACGTACACTTG
TGACCTGCAGAGCCTGGGCCTGGCTCCACTCAGGGTCCCCATCTCCATCACCATCATCCA
GGATGGAGACATCACCTGCCCTGAGGACGCCCTCGGTGCTCACCTGGAATGTCACCAAGGC
TGGCCACGTGGCACAGGCCCCATGTCTTGAGAGCAAGAGGGGCATAGTGAGGAGGCTCTG
TGGGGCTGACGGAGTCTGGGGGCCGGTCCACAGCAGCTGCACAGATGCGAGGCTCCTGGC
CTTGTTCACTAGAACCAAGCTGCTGCAGGCAGGCCAGGGCAGTCTCTGCTGAGGAGGTGCC
ACAGATCCTGGCACAGCTGCCAGGGCAGGCGGCAGAGGCAAGTTACCCCTCCGACTTACT
GACCCCTGCTGAGCACCATGAAATACGTGGCCAAGGTGGTGGCAGAGGCCAGAATACAGCT
TGACCGCAGAGCCCTGAAGAATCTCCTGATTGCCACAGACAAGGTCCTAGATATGGACAC
CAGGTCTCTGTGGACCTGGCCCCAAGCCCGGAAGCCCTGGGCAGGCTCGACTCTCCTGCT
GGCTGTGGAGACCCTGGCATGCAGCCTGTGCCCACAGGACTACCCCTTCGCCTTCAGCTT
ACCCAATGTGCTGCTGCAGAGCCAGCTGTTTGGACCCACGTTTCTGCTGACTACAGCAT
CTCCTTCCCTACTCGTCCCCCACTGCAGGCTCAGATTCCCAGGCACTCACTGGCCCCATT
GGTCCGTAAATGGAAGTGAATAAGTATTACTAGCCTGGTGTGCGAAAACCTGGACCACCT
TCTGCCCTCAAACATATGGACAAGGGCTGGGGGATTCCTCTATGCCACTCCTGGCCTGGT
CCTTGTCATTTCCATCATGGCAGGTGACCGGGCCTTCAGCCAGGGAGAGGTATCATGGA
CTTTGGGAACACAGATGGTTCCCTCACTGTGTCTTCTGGGATCACAGTCTCTTCCAGGG
CAGGGGGGGTGGTTCAAAGAAGGGTGCCAGGCACAGGTGGCCAGTGCCAGCCCCACTGC

FIGURE 7B

TCAGTGCCTCTGCCAGCACCTCACTGCCTTCTCCGTCCTCATGTCCCCACACACTGTTCC
GGAAGAACCCGCTCTGGCGCTGCTGACTCAAGTGGGCTTGGGAGCTTCCATACTGGCGCT
GCTTGTGTGCCCTGGGTGTGTACTGGCTGGTGTGGAGAGTCGTGGTGCGGAACAAGATCTC
CTATTTCCGCCACGCCGCCCTGCTCAACATGGTGTTCTGCTTGCTGGCCGCAGACACTTG
CTTCCTGGGCGCCCCATTCTCTCTCCAGGGCCCCGAAGCCCGCTCTGCCTTGCTGCCGC
CTTCCTCTGTCAATTCCTCTACCTGGCCACCTTTTCTGGATGCTGGCGCAGGCCCTGGT
GTTGGCCCACCAGCTGCTATTTGTCTTTCACCAGCTGGCAAAGCACCGAGTTCTCCCCCT
CATGGTGCTCCTGGGCTACCTGTGCCCACTGGGGTTGGCAGGTGTACCCCTGGGGCTCTA
CCTACCTCAAGGGCAATACCTGAGGGGAGGGGGAATGCTGGTTGGATGGGAAGGGAGGGGC
GTTATACACCTTCGTGGGGCCAGTGCTGGCCATCATAGGCGTGAATGGGCTGGTACTAGC
CATGGCCATGCTGAAGTTGCTGAGACCTTCGCTGTCTAGAGGGACCCCCAGCAGAGAAGCG
CCAAGCTCTGCTGGGGGTGATCAAAGCCCTGCTCATTTCTTACACCCATCTTTGGCCTCAC
CTGGGGGCTGGGCCTGGCCACTCTGTTAGAGGAAGTCTCCACGGTCCCTCATTACATCTT
CACCATTCTCAACACCCTCCAGGGCGTCTTCATCCATTGTTTGGTTGCCTCATGGACAG
GAAGATACAAGAAGCTTTGCGCAAACGCTTCTGCCGCGCCCAAGCCCCCAGCTCCACCAT
CTCCCTGGCCACAAATGAAGGCTGCATCTTGGAACACAGCAAAGGAGGAAGCGACACTGC
CAGGAAGACAGATGCTTCAGAGTGAACCACACACGGACCCATGTTCTTGCAAGGGAGTTG
AGGCTGTGTGCTTGAACCCACCAGATGAGCCCTGGCCCAATGCTCTGAACTCTTCCCGCC
TCCCGGAGCTCAGCCCTTGAGAAAGTTATGAAGAAAGGATGACTTACTTGACAGGAACCT
CTGATCTTTCAAACATTGGAGATGAAGGGCAGAATTTGGTTTGTCTTTTCAAGTTTAGGA
AAAGGTGAAGTTAATTGGTCCCTCTTCTTTAACCTTTAAAAAATCAATATAAAATGTAA
GTTTCTTAACCAT

FIGURE 8A

MTTRKLSAHSAAATPGYKAVTHKHHTGWARMAGTGLPEKGQSQAGGESGSGQLLDQENGAG
ESALVSVYVHLDLDFDKTWPELSRTLTLPAASASSSPRPLLTGLRLTTGEYMSCFEAQGF
KWNLYEVVRVPLKATDVARLPYQLSISCVTSPGFQLSCCIPSTNLAYTAAWSPGEGSKAS
SFNESGSQCFLAVQRCPMADTTYTCDLQSLGLAPLRVPISITIIQDGDITCPEDASVLT
WNVTKAGHVAQAPCPESKRGIVRRLCGADGVWGPVHSSCTDARLLALFTRTKLLQAGQGS
PAEEVPQILAQLPGQAAEASSPSDLLTLLSTMKYVAKVVAEARIQLDRRALKNLLIATDK
VLDMDTRSLWTLAQARKPWAGSTLLLA VETLACSLCPQDYPPAFSLPNVLLQSOLFQPTF
PADYSISFPTRPPLQAQIPRHSLAPLVRNGTEISITSLVLRKLDHLLPSNYGQGLGDSLY
ATPGLVLVISIMAGDRAFSQGEVIMDFGNTDGSPhCVFWDHSLFQGRGGSKEGCQAQVA
SASPTAQCLCQHLTAFSVLMSPHTVPEEPALALLTQVGLGASILALLVCLGVYWLVRV
VRNKISYFRHAALLNMVFCLLAADTCFLGAPFLSPGPRSPCLAAAFCHFLYLATFFWM
LAQALVLAHQLLFVFHQLAKHRVPLMVLLGYLCPLGLAGVTLGLYLPQGQYLREGECWL
DGKGGALYTFVGPVLAIIIGVNLVLAMAMKLLRPSLSEGPPAEKRQALLGVIKALLILT
PIFGLTWGLGLATLLEEVSTVPHYIFTILNTLQGVFILLFGCLMDRKIQEALRKRFCAQ
APSSTISLATNEGCILEHSGGSDTARKTDASE

Transmembrane domain:

573-593

609-629

648-668

685-705

728-748

770-790

803-823

N-glycosylation site.

183-186

242-245

449-452

Glycosaminoglycan attachment site.

47-50

cAMP- and cGMP-dependent protein kinase phosphorylation site.

4-7

FIGURE 8B

N-myristoylation site.

39-44

44-49

58-63

103-108

176-181

450-455

472-477

474-479

508-513

512-517

578-583

700-705

725-730

742-747

771-776

784-789

788-793

861-866

862-867

G-protein coupled receptor

231-258

642-671

727-757

771-790

578-597

811-836

7 transmembrane receptor (Secretin family)

568-828

Latrophilin/CL-1-like GPS domain

512-565

FIGURE 9

GGGAACGGAAAATGGCGCCTCACGGCCCGGGTAGTCTTACGACCCTGGTGCCCTGGGCTGCCGCCCTGCTCCTC
GCTCTGGGCGTGGAAGGGCTCTGGCGCTACCCGAGATATGCACCCAATGTCCAGGGAGCGTGCAAAATTTGTC
AAAAGTGGCCTTTTATTGTAAAACGACACGAGAGCTAATGCTGCATGCCCGTTGCTGCCTGAATCAGAAGGGCA
CCATCTTGGGGCTGGATCTCCAGAACTGTTCTCTGGAGGACCCTGGTCCAAACTTTCATCAGGCACATACCACT
GTCATCATAGACCTGCAAGCAAACCCCCCTCAAAGGTGACTTGGCCAACACCTTCCGTGGCTTTACTCAGCTCCA
GACTCTGATACTGCCACAACATGTCAACTGTCCTGGAGGAATTAATGCCTGGAATACTATCACCTCTTATATAG
ACAACCAAATCTGTCAAGGGCAAAAGAACCTTTGCAATAACACTGGGGACCCAGAAATGTGTCCTGAGAATGGA
TCTTGTGTACCTGATGGTCCAGGTCTTTTGCAGTGTGTTTGTGCTGATGGTTTCCATGGATAACAAGTGTATGCG
CCAGGGCTCGTTCTCACTGCTTATGTTCTTCGGGATTCTGGGAGCCACCACTCTATCCGTCTCCATTCTGCTTT
GGGCGACCCAGCGCCGAAAAGCCAAGACTTCATTGAACTACATAGGTCTTACCATTGACCTAAGATCAATCTGAA
CTATCTTAGCCCAGTCAGGGAGCTCTGCTTCCTAGAAAGGCATCTTTCGCCAGTGGATTGCGCTCAAGGTTGAG
GCCGCCATTGGAAGATGAAAAATTGCACTCCCTTGGTGTAGACAAATACCAGTTCCTTGGTGTGTTGCCTA
TAATAAACACTTTTTTCTTTTTTNAAAAAAAAAAAAAAAAAAAAA

FIGURE 10

Signal Peptide:

Amino acids 1-30

Transmembrane:

Amino acids 198-212

MAPHGPGSLTTLVPWAAALLLALGVERALALPEICTQCPGSVQNLSKVAFYCKTTREMLH
ARCCLNQKGTILGLDLQNCSEDPGPNFHQAHTTVIIDLQANPLKGDLANTFRGFTQLQTL
ILPQHVNCPGGINAWNTITSYIDNQICQGQKNLCNNTGDPENCPENGSCVPDGPGLLQCVC
ADGFHGYKCMRQGSFSLMFFGILGATTLSVSILLWATQRRKAKTS

FIGURE 11

GCCGCCCCGCCCCGAGACCGGGCCCGGGGCGCGGGGCGCGGGATGCGGCGCCCGGGGCG
GCGATGACCGCGGAGCGCACGCCGCGGGGCCCGGCCCTGACCCCGCCGCCCCGCGCTGAGC
CCCCCGCCGAGGTCCGGACAGGCCGAGATGACGCCGAGCCCCCTGTTGCTGCTCCTGCTGC
CGCCGCTGCTGCTGGGGGCTTCCACCGGCCCGCCGCCCCGAGGCCCCCAAGATGGC
GGACAAGGTGGTCCACGGCAGGTGGCCCCGCTGGGCCGCACTGTGCGGCTGCAGTGCCCA
GTGGAGGGGGACCCGCGCGCGCTGACCATGTGGACCAAGGATGGCCGCACCATCCACAGCG
GCTGGAGCCGCTTCCGCGTGCTGCCGAGGGGCTGAAGGTGAAGCAGGTGGAGCGGGAGGA
TGCCGCGTGTACGTGTGCAAGGCCACCAACGGCTTCGGCAGCCTGAGCGTCAACTACACC
CTCGTCTGTGCTGGATGACATTAGCCAGGGAAGGAGAGCCTGGGGCCCGACAGCTCCTCTG
GGGGTCAAGAGGACCCCGCCAGCCAGCAGTGGGCACGACCGCGCTTCACACAGCCCTCCAA
GATGAGGCGCGGGGTGATCGCACGGCCCCGTGGGTAGCTCCGTGCGGCTCAAGTGCCTGGCC
AGCGGGCACCTCTCGGCCCGACATCAGTGGATGAAGGACGACGAGCCCTTGACGCGCCAG
AGCCGCTGAGCCAGGAAGAAGAGTGGACACTGAGCCTGAAGAACCCTGCGGCCGGAGGA
CAGCGGCAATACACCTGCCGCGTGTGCAACCGCGCGGGCGCCATCAACGCCACCTACAAG
GTGGATGTGATCCAGCGGACCCGTTCCAAGCCCGTGCTCACAGGCACGCACCCCGTGAACA
CGACGGTGGACTTCGGGGGGACACGTCCTTCAGTGCAAGGTGCGCAGCGACGTGAAGCC
GGTGTCCAGTGGCTGAAGCGCGTGGAGTACGGCGCCGAGGGCCGCCAACTCCACCATC
GATGTGGGCGGCCAGAAGTTTGTGTTGCTGCCACCGGGTGACGTGTGGTGCAGCGCCGACG
GCTCCTACCTCAATAAGCTGCTCATCACCCGTGCCCGCCAGGACGATGCGGGCATGTACAT
CTGCCCTTGGCGCCAACACCATGGGGCTACAGCTTCCGCGAGCGCCTTCCTCACCGTGCTGCCA
GACCCAAAACCGCCAGGGCCACCTGTGGCCTCCTCGTCTCCTCGGCCACTAGCCTGCCGTGGC
CCGTGGTTCATCGGCATCCAGCCGGCGCTGTCTTCATCCTGGGCACCCCTGCTCCTGTGGCT
TTGCCAGGCCCAGAAGAAGCCGTGCACCCCGCGCCTGCCCTCCCCCTGCGCTGGGCACCGC
CCGCGGGGACGGCCCGCGACCGCAGCGGAGACAAGGACCTTCCCTCGTTGGCCGCCCTCA
GCGCTGGCCCTGGTGTGGGGCTGTGTGAGGAGCATGGGTCTCCGGCAGCCCCCAGCACTT
ACTGGGCCCCAGGCCAGTTGCTGGCCCTAAGTTGTACCCCAAACCTCTACACAGACATCCAC
ACACACACACACACACTCTCACACACTCACACGTGGAGGGCAAGGTCCACCAGCACA
TCCACTATCAGTGCTAGACGGCACCGTATCTGCAGTGGGCACGGGGGGCCGGCCAGACAG
GCAGACTGGGAGGATGGAGGACGGAGCTGCAGACGAAGGCAGGGGACCCATGGCGAGGAGG
AATGGCCAGCACCCAGGCAGTCTGTGTGTGAGGCATAGCCCCTGGACACACACACACAGA
CACACACACTACCTGGATGCATGTATGCACACACATGCGCGCACACGTGCTCCCTGAAGGC
ACACGTACGCACACGCACATGCACAGATATGCCGCCTGGGCACACAGATAAGCTGCCAAA
TGCATGCACACGCACAGAGACATGCCAGAACATACAAGGACATGCTGCCTGAACATACACA
CGCACACCCATGCGCAGATGTGCTGCCTGGACACACACACACACACCGGATATGCTGTCTGG
ACGCACACACGTGCAGATATGGTATCCGGACACACACGTGCACAGATATGCTGCCTGGACA
CACAGATAATGCTGCCTTGGACACACACATGCACGGATATTGCCTGGACACACACACACACA
CACGCGTGACACAGATATGCTGTCTGGACACGCACACACATGCAGATATGCTGCCTGGACAC
ACACTTCCAGACACACGTGCACAGCGCGAGATATGCTGCCTGGACACACGCAGATATGCTG
TCTAGTCACACACACACGCAGACATGCTGTCCGGACACACACACGCATGCACAGATATGCT
GTCCGGACACACACACGCACGCAGATATGCTGCCTGGACACACACACAGATAATGCTGCCT
CAACACTCACACACGTGCAGATATTGCCTGGACACACACATGTGCACAGATATGCTGTCTG
GACATGCACACACGTGCAGATATGCTGTCCGGATACACACGCACGCACACATGCAGATATG
CTGCCTGGGCACACACTTCCGGACACACATGCACACACAGGTGCAGATATGCTGCCTGGAC
ACACACACAGATAATGCTGCCTCAACACTCACACACGTGCAGATATTGCCTGGACACACAC
ATGTGCACAGATATGCTGTCTGGACATGCACACACGTGCAGATATGCTGTCCGGATACACA
CGCACGCACACATGCAGATATGCTGCCTGGGCACACACTTCCGGACACACATGCACACACA
GGTGCAGATATGCTGCCTGGACACACGCAGACTGACGTGCTTTTGGGAGGGTGTGCCGTGA
AGCCTGCAGTACGTGTGCCGTGAGGCTCATAGTTGATGAGGGACTTCCCTGCTCCACCGT
CACTCCCCCAACTCTGCCCGCCTCTGTCCCCGCTCAGTCCCCGCTCCATCCCCGCCTCT
GTCCCCCTGGCCTTGGCGGCTATTTTGGCCACCTGCCTTGGGTGCCCAGGAGTCCCCTACTG
CTGTGGGCTGGGGTTGGGGGCACAGCAGCCCCAAGCCTGAGAGGCTGGAGCCCATGGCTAG
TGGCTCATCCCCAGTGCACTTCTCCCCCTGACACAGAGAAGGGGCCTTGGTATTTATATTTA
AGAAATGAAGATAATATTAATAATGATGAAGGAAGACTGGGTTGCAGGGACCTGTGGTCTC
TCCTGGGGCCCGGACCCGCTGTGCTTTTCAGCCATGCTGATGACCACCCCGTCCAGGC
CAGACACCACCCCCCACTGTGCTGGTGGCCCCAGATCTCTGTAATTTTATGTAGAG
TTTGAGCTGAAGCCCCGTATATTTAATTTATTTTGTAAACACAAAA

FIGURE 12

MTPSPLLLLLLLPLLLLGAFPPAAAARGPPKMADKVVP RQVARLGRTVRLQCPVEGDPPPLT
MWTKDGR TIHSGWSRFRVLPQGLKVKQVEREDAGVYVCKATNGFGSLSVNYTLVVLDDISP
GKESLGPDSSSGGQEDPASQQWARPRFTQPSKMRRRV IARPVGSSVRLKCVASGHPRPDIT
WMKDDQALTRPEAAEPRKKKWTLSLKNLRPEDSGKYTCRV SNRAGAINATYKVDVIQRTS
KPVLTGTHPVNTTVDFGGTTSFQCKVRSDVKPVIQWLKRVEYGAEGRHNSTIDVGGQKFVV
LPTGDVWSRPDGSYLNKLLITRARQDDAGMYICLGANTMGYSFRSAFLT VLPDPKPPGPPV
ASSSSATSLPWPV VIGIPAGAVFILGTLLLWLCQAQKKPCTPAPAPPLPGHRPPGTARDS
GDKDLPSLAALSAGPGVGLCEEHGSPAAPQHLLGPGPVAGPKLYPKLYTDIHTHTHTHSHT
HSHVEGKVHQHIHYQC

FIGURE 13

CGGACGCGTGGGCGTCCGGCGGTGCGCAGAGCCAGGAGGCGGAGGCGCGCGGGCCAGCCTGG
GCCCCAGCCACACCTTCACCAGGGCCCAGGAGCCACCATGTGGCGATGTCCACTGGGGCT
ACTGCTGTTGCTGCCGCTGGCTGGCCACTTGGCTCTGGGTGCCAGCAGGGTCGTGGGCGC
CGGGAGCTAGCACCGGGTCTGCACCTGCGGGGCATCCGGGACGCGGGAGGCCGGTACTGCC
AGGAGCAGGACCTGTGCTGCCGCGGCCGTGCCGACGACTGTGCCCTGCCCTACCTGGGCGC
CATCTGTTACTGTGACCTCTTCTGCAACCGCACGGTCTCCGACTGCTGCCCTGACTTCTGG
GACTTCTGCCTCGGCGTGCCACCCCTTTTCCCCCGATCCAAGGATGTATGCATGGAGGTC
GTATCTATCCAGTCTTGGGAACGTACTGGGACAACTGTAACCGTTGCACCTGCCAGGAGAA
CAGGCAGTGGCATGGTGGATCCAGACATGATCAAAGCCATCAACCAGGGCAACTATGGCTG
GCAGGCTGGGAACCAAGCGCCTTCTGGGGCATGACCCTGGATGAGGGCATTTCGCTACCGC
CTGGGACCATCCGCCCATCTTCTCGGTTCATGAACATGCATGAAATTTATACAGTGCTGA
ACCCAGGGGAGGTGCTTCCACAGCCTTCGAGGCCTCTGAGAAGTGGCCCAACCTGATTCA
TGAGCCTCTTGACCAAGGCAACTGTGCAGGCTCCTGGGCCTTCTCCACAGCAGCTGTGGCA
TCCGATCGTGTCTCAATCCATTCTCTGGGACACATGACGCCTGTCTGTGCCCCAGAACC
TGCTGTCTTGTGACACCCACCAGCAGCAGGGCTGCCGCGGTGGGCGTCTCGATGGTGCCTG
GTGGTTCTTGTGCTCGCCGAGGGGTGGTGTCTGACCACTGCTACCCCTTCTCGGGCCGTGAA
CGAGACGAGGCTGGCCCTGCGCCCCCTGTATGATGCACAGCCGAGCCATGGGTGCGGGCA
AGCGCCAGGCCACTGCCCCACTGCCCCAACAGCTATGTTAATAACAATGACATCTACCAGGT
CACTCCTGTCTACCGCCTCGGCTCCAACGACAAGGAGATCATGAAGGAGCTGATGGAGAAT
GGCCCTGTCCAAGCCCTCATGGAGGTGCATGAGGACTTCTTCTTATAACAAGGGAGGCATCT
ACAGCCACACGCCAGTGAGCCTTGGGAGGCCAGAGAGATAACCGCCGGCATGGGACCCACTC
AGTCAAGATCACAGGATGGGGAGAGGAGACGCTGCCAGATGGAAGGACGCTCAAATACTGG
ACTGCGGCCAACTCCTGGGGCCCAGCCTGGGGCGAGAGGGGCCACTTCCGCATCGTGC GCG
GCGTCAATGAGTGCGACATCGAGAGCTTCGTGCTGGGCGTCTGGGGCCGCGTGGGCATGGA
GGACATGGGTTCATCACTGAGGCTGCGGGCACACGCGGGGTCCGGCCTGGGATCCAGGCTA
AGGGCCGGCGGGAAGAGGCCCAATGGGGCGGTGACCCAGCCTCGCCCGACAGAGCCCGGG
GCGCAGGCGGGCGCCAGGGCGCTAATCCCGGCGCGGGTTCCGCTGACGCAGCGCCCCGCCT
GGGAGCCGCGGGCAGGCGAGACTGGCGGAGCCCCAGACCTCCAGTGGGGACGGGGCAGG
GCCTGGCCTGGGAAGAGCACAGCTGCAGATCCCAGGCCTCTGGCGCCCCCACTCAAGACTA
CCAAAGCCAGGACACCTCAAGTCTCCAGCCCCAATACCCCAACCCCAATCCCGTATTCTTTT
TTTTTTTTTTTTTAGACAGGGTCTTGCTCCGTTGCCAGGTTGGAGTGCAGTGGCCCATCAG
GGCTCACTGTAACCTCCGACTCCTGGGTTCAGTGACCTCCACCTCAGCCTCTCAAGTA
GCTGGGACTACAGGTGCACCACCACACCTGGCTAATTTTTGTATTTTTTGTAAAGAGGGGG
GTCTCACTGTGTTGCCAGGCTGGTTTCGAACTCCTGGGCTCAAGCGGTCCACCTGCCTCC
GCCTCCCAAAGTGCTGGGATTGCAGGCATGAGCCACTGCACCCAGCCCTGTATTCTTATTC
TTCAGATATTTATTTTTCTTTTCACTGTTTTTAAAATAAAACCAAAGTATTGATAAAAAAAA

FIGURE 14

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA33223

><subunit 1 of 1, 164 aa, 1 stop

><MW: 18359, pI: 7.45, NX(S/T): 1

MWRCPLGLLLLLLPLAGHLALGAQQGRGRRELAPGLHLRGIRDAGGRYCQEQLCCRGRADD
CALPYLGAICYCDLFCNRTVSDCCPDFWDFCLGVPPFPFPPIQGCMHGGRIYPVLGTYWDNC
NRCTCQENRQWHGGSRHDQSHQPGQLWLAGWEPQRLLGHDPG

N-glycosylation site.

amino acids 78-82, 161-165

Casein kinase II phosphorylation site.

amino acids 80-84, 117-121, 126-130, 169-173, 205-209, 296-300,
411-415

N-myristoylation site.

amino acids 21-27, 39-45, 44-50, 104-110, 160-164, 224-230,
269-275, 378-384, 442-448

Amidation site.

amino acids 26-30, 318-322

Eukaryotic thiol (cysteine) proteases histidine active site.

amino acids 398-409

FIGURE 15

GGCTCAGAGGCCCACTGGACCCTCGGCTCTTCCTTGGACTTCTTGTTGTGTTCTGTGAGCTTCGCTGGATTTCAG
GGTCTTGGGCATCAGAGGTGAGAGGGTGGGAAGGTCCGCCGCGATGGGGAAGCCCTGGCTGCGTGCGCTACAGC
TGCTGCTCCTGCTGGGCGCGTCGTGGGCGCGGGCGGGCGCCCCGCGCTGCACCTACACCTTCGTGCTGCCCCCG
CAGAAGTTCACGGGCGCTGTGTGCTGGAGCGGCCCCGCATCCACGCGGGCGACGCCCGAGGCCGCCAACGCCAG
CGAGCTGGCGGCGCTGCGCATGCGCGTCGGCCGCCACGAGGAGCTGTTACGCGAGCTGCAGAGGCTGGCGGCGG
CCGACGGCGCCGTGGCCGGCGAGGTGCGCGCGCTGCGCAAGGAGAGCCCGCGGCTGAGCGCGCGCCTGGGCCAG
TTGCGCGCGCAGCTGCAGCACGAGGCGGGGCCCCGGGGCGGGCCCCGGGGCGGATCTGGGGGCGGAGCCTGCCGC
GGCGCTGGCGCTGCTCGGGGAGCGCGTGTCTCAACGCGTCCGCCGAGGCTCAGCGCGCAGCCGCCCGTTCCACC
AGCTGGACGTCAAGTTCGCGAGCTGGCGCAGCTCGTCACCCAGCAGAGCAGTCTCATCGCCCGCCTGGAGCGC
CTGTGCCCGGGAGGCGCGGGCGGGCAGCAGCAGGTCTGCGGCCACCCCCACTGGTGCTGTGGTTCCGGTCCG
TCTTGTGGGTAGCACCACTGACACCAGTAGGATGCTGGACCCAGCCCCAGAGCCCCAGAGAGACCAGACCCAGA
GACAGCAGGAGCCCATGGCTTCTCCCATGCCTGCAGGTACCCCTGCGGTCCCCACCAAGCCTGTGGGCCCGTGG
CAGGATTGTGCAGAGGCCCGCCAGGCAGGCCATGAACAGAGTGGAGTGTATGAACTGCGAGTGGGCCGTCACGT
AGTGTCAGTATGGTGTGAGCAGCAACTGGAGGGTGGAGGCTGGACTGTGATCCAGCGGAGGCAAGATGGTTTCAG
TCAACTTCTTCACTACCTGGCAGCACTATAAGGCGGGCTTTGGGCGGCCAGACGAGAATACTGGCTGGGCCTT
GAACCCGTGTATCAGCTGACCAGCCGTGGGGACCATGAGCTGCTGGTTCTCCTGGAGGACTGGGGGGGCCGTGG
AGCACGTGCCCACTATGATGGCTTCTCCCTGGAACCCGAGAGCGACCACTACCGCCTGCGGCTTGGCCAGTACC
ATGGTGATGCTGGAGACTCTCTTTCCTGGCACAAATGACAAGCCCTTCAGCACCGTGGATAGGGACCGAGACTCC
TATTCTGGTAACTGTGCCCTGTACCAGCGGGGAGGCTGGTGGTACCATGCCTGTGCCCACTCCAACCTCAACGG
TGTGTGGCACCACGGCGGCCACTACCGAAGCCGCTACCAGGATGGTGTCTACTGGGCTGAGTTTCGTGGTGGGG
CATATTCTCTCAGGAAGGCCGCCATGCTCATTCGGCCCCCTGAAGCTGTGACTCTGTGTTCTCTGTCCCCCTAGG
CCCTAGAGGACATTGGTCAGCAGGAGCCCAAGTTGTTCTGGCCACACCTTCTTTGTGGCTCAGTGCCAATGTGT
CCCACAGAACTTCCCACTGTGGATCTGTGACCCTGGGCGCTGAAAATGGGACCCAGGAATCCCCCCCCGTCAATA
TCTTGGCCTCAGATGGCTCCCCAAGGTCATTTCATATCTCGGTTTGAGCTCATATCTTATAATAACACAAAGTAG
CCAC

FIGURE 16

Signal sequence: Amino acids 1-20

N-glycosylation sites: Amino acids 58-62;145-149

cAMP- and cGMP-dependent protein kinase phosphorylation site:
Amino acids 97-101

Tyrosine kinase phosphorylation site: Amino acids 441-448

N-myristoylation sites: Amino acids 16-22;23-29;87-93;
108-114;121-127;125-131;129-135;
187-193;293-299;353-359;378-384;
445-451;453-459

Cell attachment sequence: Amino acids 340-343

Fibrinogen beta and gamma chains C-terminal domain signature:
Amino acids 418-431

MGKPWLRLALQLLLLLLGASWARAGAPRCTYTFVLPPQKFTGAVCWSGPASTRATPEAANASE
LAALRMRVGRHEELLRELQRLAAADGAVAGEVRALRKESRGLSARLGQLRAQLQHEAGPGA
GPGADLGAEPAAALALLGERVLNASAEAQRAAARFHQLDVKFRELAQLVTQQSSLIARLER
LCPGGAGGQQQVLPPPPLVPVVPVRLVGSTSDTSRMLDPAPEPQRDQTQRQQEPMASMPMA
GHPAVPTKPVGPWQDCAEARQAGHEQSGVYELRVGRHVSVWCEQQLEGGGWTVIQRQDQD
SVNFFTTWQHYKAGFGRPDGEYWLGLEPVYQLTSRGDHELLVLLEDWGGRGARAHYDGFSL
EPESDHYRLRLGQYHGDAGDSL SWHNDKPFSTVDRDRDSYSGNCALYQRGGWYHACAHSN
LNGVWHHGGHYRSRYQDGVYWAEFRGGAYSLRKAAMLIRPLKL

FIGURE 17

AGCCCACCGAGAGGCGCCTGCAGGATGAAAGCTCTCTGTCTCCTCCTCCTCCCTGTCCTGGGGCTGTTGGTGTC
TAGCAAGACCCTGTGCTCCATGGAAGAAGCCATCAATGAGAGGATCCAGGAGGTCGCCGGCTCCCTAATATTTA
GGGCAATAAGCAGCATTGGCCTGGAGTGCCAGAGCGTCACCTCCAGGGGGGACCTGGCTACTTGCCCCCGAGGC
TTCGCCGTCACCGGCTGCACTTGTGGCTCCGCCTGTGGCTCGTGGGATGTGCGCGCCGAGACCACATGTCACTG
CCAGTGCGCGGGCATGGACTGGACCGGAGCGCGCTGCTGTCTGTGTCAGCCC TGAGGTCGCGCGCAGCGCGTGC
ACAGCGCGGGCGGAGGCGGCTCCAGGTCCGGAGGGGTTGCGGGGGAGCTGGAAATAAACCTGGAGATGATGATG
ATGATGATGATGGAAAA

FIGURE 18

MKALCLLLLLPVLGLLVSSKTLCSMEEAINERIQEVAGSLIFRAISSIGLEQSVTSRGD
LATCPRGFAVTGCTCGSACGSWDVRAETTCHCQCAGMDWTGARCCRVQP

Signal peptide:

1-18

Transmembrane domain:

none

Cell attachment sequence.

57-60

N-myristoylation site.

13-19

71-77

75-81

95-101

100-106

FIGURE 19A

```

1  tcaggggtcag gtgattctcc cacctcagcc tcctgagtag ctgggagtag aggcacatgc
61  caccacacccc agataatttt taaatttttt gtagagatgg ggtctcactg tgttgcccag
121 gctgggtctcg agctcctggg ctgaagtgat ccatccacct cgtccacca aagtgctggg
181 attacagggtg tgagccaccg tgccctgoot gcatttcttt taatagacat gtctctggat
241 ggtcaactgg acagttgtgc tcaccctcca catttctctc cctctactca caccccaagg
301 tgataatgga ttggcaaccc tgggtgactt aagaattcca tgagcttcat aaatgtcaaa
361 taagctgtct taccctacta acccctctac catcacaatg atcaaagcaa agccaaatag
421 cccacacctc tcatcccaca cataccatag tcatcctttc atccatttat ccatccattt
481 accaacttaa aatattcatt gattacctac tacatatgac actttacttg accaaaattg
541 gcaaaacaca tagcttaaag ttgtctttct tcctagttag gtggaatgat gcctgggtata
601 tcgtatcatt agaaatggct gaatgaatga gctcactgtt tattaggaga atgagacaca
661 gaccaaataa ctcaagcata agagagaatg tagttagtgt cctaaaagag atccagagtg
721 ctgtgtgagt tcaaagggtg gaaagagccc ttctgactga agaaatcagg aaagacttca
781 tagaagcagt ggtgatatat gagctgactt ctaaaggaca agtaagatta taatagcaga
841 tatagtaggg gaagggaatt accgaggggg tggcatcaat aaagttttgg gggtaaggaa
901 gtatgagttc tgggtatgaa aatatgtcta acttggtcag agcataaatt acgtattctg
961 gaaggtagac tgtgtttgag aacaaatgct agaatacctt aaaagctaatt ttgttagggt
1021 ctgcagagtc agtgatagga cccaagcaga caagtaatta ggaagactaa tttggcaagg
1081 atattataaa atgttggggc tgaacaatta ttacatataa taagagaatt aacaagggtc
1141 ctgagtgaaa tgtaataaac agaaaacaac aaattttgta tgtcaaccaa acctagcagt
1201 caaaaggatt aataacaata agtcatgtag gatactatga attcataaca caaagaaatg
1261 ctaggggaaa tatttgcaat gcttatcaca tccaaaagtt ctttcccta atatacaaag
1321 atctgctaga agtcaacaag ctaaagatca acagctcaat agaaatatgg ccaaacggct
1381 ggacgtggtg gctcatgcct gtaatcccag cattttggga gactgaggca ggattgcttg
1441 agcccaggaa ttcaagacca gcctgggtcaa cgtagcgaga ttctgtgtct atatttttaa
1501 aaattttatta aaaaaagaaa tacgggcaaa tgagctacct agtctcagaa aagaaaatat
1561 atatgatgtg caactatatt aaaagatttt caatttctact aataattttt ttttttgaga
1621 cagagtcttg ctctgtcgcc aggctggagt gcagtggcac catcttggct cactgcaagc
1681 tctgcctccc gagttcacca ttctcctgcc tcagcctccc aagtagctgg gattacaggc
1741 gcacaccacc acacctggct aatgttttgt attttttagta gaggcggggg ttcaccgtgt
1801 tagccaggat ggctcgatc tcttgacctc gtgatcagcc caccttggcc tctcaaagtg
1861 ctgtgattac aggcgtgagc caccgcgcct ggccaaattt cactaataat tttaaaaagt
1921 aaattatata tacatgggat atcatgttca cttagattgg cgatgagcag aaagtttgat
1981 aactgtgtca taaacacttg gtaactgtgt tagtgagtgt gtggggagat aggtatcctt
2041 atatgctgct aataggagtg taggctgtaa aattctcatg gtagctagtt tagcaatatc
2101 tataaaaatt acaaatatgc ataactttca gtgagtcaga aattttactt ttaagaattt

```

FIGURE 19B

2161 atcttacatg tataatcaca acacgtgtga aatatcgtac acataataga tattgggttgc
2221 aatctttttca tagttgtgaa agatgaggaa aaacaatctt aaaagtagtt tggttaaata
2281 aatcatgtca ctcatataca gtgaaatata atccccatctt taaaaagatg atgggtggtgg
2341 tgctatacat accgatacag aaagctttct aaaacctttc attaaatgaa aaatgaataa
2401 atcattgcag aacagtgtat atatatctaa aatatctatg gaagaaacca gcaacagcca
2461 ctgctcctgg agaattatgg tcccacacca ctgatcattc tttcagtagg gtgaccatca
2521 tccaaatttg cttgggactg aggggggttcc ttttggtttg aaaaccagga cagtcctagg
2581 aaaagtgaga caagttgggc acatgtcccc aagatgatct tctttcactt atgaacttgc
2641 tactttccca gtcagaatat aaactctgag gggggagact tcctgttttc ttcattgacta
2701 tatctcttgc gcactgtggg gtggaggctg tagaagagga gagaagtaga gaaacagatc
2761 acatttgtgc ttgaagtgtt tcagcaaata tgggcaacac ctttctttta ctagcttgga
2821 accctacctc tgagtgcatt tcccttttta ttattttattt cctgtcagtt ataagagagg
2881 cctacccctt tgtgagcagt ctaggacttt gtacacctgc taagtaggga gaaggcaggg
2941 gaggtggctg gtttaagggg aacttgaggg aagtagggaa gactcctctc gggacctttg
3001 gagtaggtga cacatgagcc cagccccagc tcacctgcca atccagctga ggagctcacc
3061 tgccaatcca gctgaggctg ggcagagggtg ggtgagaaga gggaaaattg cagggacctc
3121 cagttgggcc aggccagaag ctgctgtagc ttttaaccaga cagctcagac ctgtatggag
3181 gctgccagtg acagggttagg tttagggcag agaagaagca agacctg

FIGURE 20

MVGKMWPVLWTLCAVRVTVDALSVETPQDVLRSQGKSVTLPCITYHTSTSSREGLIQWDKLLLTHTERVVIWPF
SNKNYIHGELYKNRVSI SNNAEQSDASITIDQLTMADNGTYECSVSLMSDLEGNTKSRVRLLVLPVPPSKPECGI
EGETIIGNNIQLTCQSKEGSPTPQYSWKRYNILNQEQLAQPASGQPVSLKNISTDTSGYYICTSSNEEGTQFC
NITVAVRSPSMNVALYVGIAVGVVAALIIIGIIIIYCCCRGKDDNTEDKEDARPNREAYEEPPEQLRELSRERE
EEDDYRQEEQRSTGRES PDHLDQ

FIGURE 21A

CGCGGAGCCCTGCGCTGGGAGGTGCACGGTGTGCACGCTGGACTGGACCCCATGCAACCCGCGCCCTGCGCC
TTAACCAGGACTGCTCCGCGCGCCCTGAGCCTCGGGCTCCGGCCCGGACCTGCAGCCTCCAGGTGGCTGGGA
AGAACTCTCCAACAATAAATACATTTGATAAGAAAGATGGCCTTTAAAAGTGCTACTAGAACAAGAGAAAACGTT
TTTCACTCTTTTAGTATTACTAGGCTATTTGTTCATGTAAAGTGACTTGTGAATCAGGAGACTGTAGACAGCAAG
AATTTCAGGGATCGGTCTGGAACTGTGTTCCCTGCAACCAGTGTGGGCCAGGCATGGAGTTGTCTAAGGAATGT
GGCTTCGGCTATGGGGAGGATGCACAGTGTGTGACGTGCCGGCTGCACAGGTTCAAGGAGGACTGGGGCTTCCA
GAAATGCAAGCCCTGTCTGGACTGCGCAGTGGTGAACCGCTTTCAGAAGGCAAATTTGTTTCAGCCACCAGTGATG
CCATCTGCGGGGACTGCTTGCCAGGATTTTATAGGAAGACGAAACTTGTGCGCTTTCAGACATGGAGTGTGTG
CCTTGTGGAGACCCCTCCTCCTCCTTACGAACCGCACTGTGCCAGCAAGGTCAACCTCGTGAAGATCGCGTCCAC
GGCCTCCAGCCACGGGACACGGCGCTGGCTGCCGTTATCTGCAGCGCTCTGGCCACCGTCTGTGCGCCCTGC
TCATCCTCTGTGTTCATCTATTGTAAGAGACAGTTTATGGAGAAGAAACCCAGCTGGTCTCTGCGGTGCGCAGGAC
ATTCAGTACAACGGCTCTGAGCTGTCTGTGTTTTGACAGACCTCAGCTCCACGAATATGCCACAGAGCCTGCTG
CCAGTGCCCGCGTGACTCAGTGCAGACCTGCGGGCCGGTGCGCTTGCTCCCATCCATGTGTCTGTGAGGAGGCCCT
GCAGCCCCAACCCGGCGACTCTTGTTGTGGGGTGCACTTCTGCAGCCAGTCTTCAGGCAAGAAACGCAGGCCCA
GCCGGGGAGATGGTGCCGACTTTCTTCGGATCCCTCACGCAGTCCATCTGTGGCGAGTTTTCAGATGCCTGGCC
TCTGATGCAGAATCCCATGGGTGGTGACAACATCTCTTTTTGTGACTCTTATCCTGAACTCACTGGAGAAGACA
TTCATTCTCTCAATCCAGAACTTGAAAGCTCAACGTCTTTGGATTCAAATAGCAGTCAAGATTTGGTTGGTGGG
GCTGTTCCAGTCCAGTCTCATTCTGAAAACTTTACAGCAGCTACTGATTTATCTAGATATAACAACACACTGGT
AGAATCAGCATCAACTCAGGATGCATAACTATGAGAAGCCAGCTAGATCAGGAGAGTGGCGCTGTTCATCCACC
CAGCCACTCAGACGTCCCTCCAGGAAGCTTAAAGAACCTGCTTCTTTCTGCAGTAGAAGCGTGTGCTGGAACCC
AAAGAGTACTCCTTTGTAGGCTTATGGACTGAGCAGTCTGGACCTTGCAATGGCTTCTGGGGCAAAAATAAATC
TGAACCAAACCTGACGGCATTGTAAGCCTTTCAGCCAGTTGCTTCTGAGCCAGACCAGCTGTAAGCTGAAACCTC
AATGAATAACAAGAAAAGACTCCAGGCCGACTCATGATACTCTGCATCTTTCTACATGAGAAGCTTCTCTGCCAC
AAAAGTGACTTCAAAGACTGATGGGTGAGCTGGCAGCCTATGAGATTGTGGACATATAACAAGAAACAGAAAT
GCCCTCATGCTTATTTTCATGGTGATTGTGGTTTTACAAGACTGAAGACCCAGAGTATACTTTTTCTTTCCAGA
AATAATTTTCATACCGCCTATGAAATATCAGATAAATTACCTTAGCTTTTATGTAGAATGGGTTCAAAAGTGAGT
GTTTCTATTTGAGAAGGACACTTTTTTCATCATCTAAACTGATTTCGCATAGGTGGTTAGAATGGCCCTCATATTG
CCTGCCCTAAATCTTGGGTTTATTAGATGAAGTTTACTGAATCAGAGGAATCAGACAGAGGAGGATAGCTCTTTC
CAGAATCCACACTTCTGACCTCAGCCTCGGTCTCATGAACACCCGCTGATCTCAGGAGAACACCTGGGCTAGGG
AATGTGGTCGAGAAAGGGCAGCCCATTGCCAGAAATTAACACATATTGTAGAGACTTGTATGCAAAGGTTGGCA
TATTTATATGAAAATTAGTTGCTATAGAAACATTTGTTGCATCTGTCCCTCTGCCTGAGCTTAGAAGGTTATAG
AAAAAGGGTATTTATAAACATAAATGACCTTTTACTTGCATTGTATCTTATACTAAAGGCTTTAGAAATTACAA
CATATCAGGTTCCCTACTACTGAAGTAGCCTTCCGTGAGAACACACCACATGTTAGGACTAGAAGAAAATGCA
CAATTTGTAGGGGTTTGGATGAAGCAGCTGTAACCTGCCCTAGTGTAGTTTGACCAGGACATTGTCTGTCTCCTT
CCAATTGTGTAAGATTAGTTAGCACATCATCTCTACTTTAGCCATCCGGTGTGGATTAAAGAGGACGGTGCT
TCTTCTATTAAAGTGCTCCATCCCTACCATCTACACATTAGCATTGTCTCTAGAGCTAAGACAGAAATTAAC

FIGURE 21B

CCCGTTCAGTCACAAAGCAGGGAATGGTTCATTTACTCTTAATCTTTATGCCCTGGAGAAGACCTACTTGAACA
GGGCATATTTTTTAGACTTCTGAACATCAGTATGTTGAGGGTACTATGATATTTGGTTTGGAATTGCCCTGC
CCAAGTCACTGTCTTTTAACTTTTAACTGAATATTAAAATGTATCTGTCTTTCCT

FIGURE 22

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA84210

><subunit 1 of 1, 417 aa, 1 stop

><MW: 45305, pI: 5.12, NX(S/T): 6

MALKVLLLEQEKTFFTLVLLGYLSCKVTCESGDCRQQEFRDRSGNCVPCNQCGPGMELSK
ECGFGYGEDAQCVTCLHRFKEDWGFQKCKPCLDCAVVNRFQKANCSATSDAICGDCLPG
FYRKTKLVGFQDMECVPCGDP PPPPYEPHCASKVNLVKIASTASSPRDTALAAVICSLAT
VLLALLILCVIYCKRQFMEKKPSWSLRSQDIQYNGSELSCFDRPQLHEYAHRACCQCRD
SVQTCGPVRLLLPSMCCEEACSPNPATLGC GVHSAASLQARNAGPAGEMVPTFFGSLTQSI
CGEFSDAWPLMQNPMGGDNISFCDSYPELTGEDIHSLNPELESSTSLDSNSSQDLVGGAV
PVQSHSENFTAATDLSRYNNTLVESASTQDALTMRSQLDQESGAVIHPATQTSLQEA

FIGURE 23A

CGCGCTCCCCGCGCGCCTCCTCGGGCTCCACGCGTCTTGCCCCGCAGAGGCAGCCTCCTCCAGGAGCGGGGCCC
TGCACACCATGGCCCCCGGGTGGGCAGGGGTGCGCGCCGCGTGCGCGCCCGCTGGCGCTGGCCTTGCGCTG
GCGAGCGTCCCTGAGTGGGCCTCCAGCCGTGCGCTGCCCCACCAAGTGTACCTGCTCCGCTGCCAGCGTGGACTG
CCACGGGCTGGGCCTCCGCGCGGTTCTTCGGGGCATCCCCGCAACGCTGAGCGCCTTGACCTGGACAGAAATA
ATATCACCAGGATCACCAGATGGACTTCGCTGGGCTCAAGAACCTCCGAGTCTTGCACTTGGAAGACAACCAG
GTCAGCGTCATCGAGAGAGGCGCCTTCCAGGACCTGAAGCAGCTAGAGCGACTGCGCCTGAACAAGAATAAGCT
GCAAGTCCTTCCAGAATTGCTTTTCCAGAGCACGCCGAAGCTCACCAGACTAGATTTGAGTGAAAACCAGATCC
AGGGGATCCCCGAGGAAGGCGTTCCGCGGCATCACCAGTGTGAAGAACCTGCAACTGGACAACAACCACATCAGC
TGCAATTGAAGATGGAGCCTTCCGAGCGCTGCGCGATTGGAGATCCTTACCCTCAACAACAACAACATCAGTCG
CATCCTGGTCCAGCTTCAACCACATGCCGAAGATCCGAACCTTGCGCCTCCACTCCAACCACCTCTACTGCG
ACTGCCACCTGGCCTGGCTCTCGGATTGGCTGCGACAGCGACGGACAGTTGGCCAGTTCACACTCTGCATGGCT
CCTGTGCATTTGAGGGGCTTCAACGTGGCGGATGTGCAGAAGAAGGAGTACGTGTGCCAGCCCCCACTCGGA
GCCCCCATCCTGCAATGCCAACTCCATCTCCTGCCCTTCGCCCTGCACGTGCAGCAATAACATCGTGGACTGTC
GAGGAAAGGGCTTGATGGAGATTCTGCCAACTTGCCGGAGGGCATCGTCGAAATACGCCCTAGAACAGAACTCC
ATCAAAGCCATCCCTGCAGGAGCCTTCACCCAGTACAAGAACTGAAGCGAATAGACATCAGCAAGAATCAGAT
ATCGGATATTGCTCCAGATGCCTTCCAGGGCCTGAAATCACTCACATCGCTGGTCTGTATGGGAACAAGATCA
CCGAGATTGCCAAGGGACTGTTTGATGGGCTGGTGTCCCTACAGCTGCTCCTCCTCAATGCCAACAAGATCAAC
TGCTGCGGGTGAACACGTTTCAGGACCTGCAGAACCTCAACTTGCTCTCCTGTATGACAACAAGCTGCAGAC
CATCAGCAAGGGGCTCTTCGCCCCCTCTGCAGTCCATCCAGACACTCCACTTAGCCCCAAAACCCATTTGTGTGCG
ACTGCCACTTGAAGTGGCTGGCCGACTACCTCCAGGACAACCCCATCGAGACAAGCGGGGCCGCTGCAGCAGC
CCGCGCCGACTCGCCAACAAGCGCATCAGCCAGATCAAGAGCAAGAAGTTCCGCTGCTCAGGCTCCGAGGATTA
CCGAGCAGGTTTCAGCAGCGAGTGCTTCATGGACCTCGTGTGCCCCGAGAAGTGTGCTGTGAGGGCACGATTG
TGGACTGCTCCAACCAGAAGCTGGTCCGCATCCCAAGCCACCTCCCTGAATATGTCACCGACCTGCGACTGAAT
GACAATGAGGTATCTGTTCTGGAGGCCACTGGCATCTTCAAGAAGTTGCCCAACCTGCGGAAAATAAATCTGAG
TAACAATAAGATCAAGGAGGTGCGAGAGGGAGCTTTTCGATGGAGCAGCCAGCGTGCAGGAGCTGATGCTGACAG
GGAACCAGCTGGAGACCGTGCACGGGCGCGTGTTCGCTGGCCTCAGTGGCCTCAAACCTTGATGCTGAGGAGT
AACTTGATCAGCTGTGTGAGTAATGACACCTTTGCCGGCCTGAGTTCGGTGAGACTGCTGTCCCTCTATGACAA
TCGGATCACCACCATCACCCCTGGGGCCTTCACCACGCTTGTCTCCCTGTCCACCATAAACCTCCTGTCCAACC
CCTTCAACTGCAACTGCCACCTGGCCTGGCTCGGCAAGTGGTTGAGGAAGAGGCGGATCGTCAGTGGGAACCTT
AGGTGCCAGAAGCCATTTTTCTCAAGGAGATTCCCATCCAGGATGTGGCCATCCAGGACTTCACCTGTGATGG
CAACGAGGAGAGTAGCTGCCAGCTGAGCCCGCGCTGCCCGGAGCAGTGACCTGTATGGAGACAGTGGTGCAT
GCAGCAACAAGGGGCTCCGCGCCCTCCCCAGAGGCATGCCCAAGGATGTGACCGAGCTGTACCTGGAAGGAAAC
CACCTAACAGCCGTGCCAGAGAGCTGTCCGCCCTCCGACACCTGACGCTTATTGACCTGAGCAACAACAGCAT
CAGCATGCTGACCAATTACACCTTCAGTAACATGTCTCACCTCTCCACTCTGATCCTGAGCTACAACCGGCTGA
GGTGCATCCCCGTCCACGCCTTCAACGGGCTGCGGTCCCTGCGAGTGCTAACCTCCATGGCAATGACATTTCC
AGCGTTCTTGAAGGCTCCTTCAACGACCTCACATCTCTTCCCATCTGGCGCTGGGAACCAACCCACTCCACTG

FIGURE 23B

TGACTGCAGTCTTCGGTGGCTGTCGGAGTGGGTGAAGGCGGGGTACAAGGAGCCTGGCATCGCCCGCTGCAGTA
GCCCTGAGCCCATGGCTGACAGGCTCCTGCTCACCACCCCAACCCACCGCTTCCAGTGCAAAGGGCCAGTGGAC
ATCAACATTGTGGCCAAATGCAATGCCTGCCTCTCCAGCCCGTGCAAGAATAACGGGACATGCACCCAGGACCC
TGTGGAGCTGTACCGCTGTGCCTGCCCCACAGCTACAAGGGCAAGGACTGCCTGTGCCCATCAACACCTGCA
TCCAGAACCCCTGTGAGCATGGAGGCACCTGCCACCTGAGTGACAGCCACAAGGATGGGTTCAGCTGCTCCTGC
CCTCTGGGCTTTGAGGGGCAGCGGTGTGAGATCAACCCAGATGACTGTGAGGACAACGACTGCGAAAACAATGC
CACCTGCGTGGACGGGATCAACAACCTACGTGTGTATCTGTCCGCCTAACTACACAGGTGAGCTATGCGACGAGG
TGATTGACCACTGTGTGCCTGAGCTGAACCTCTGTGAGCATGAGGCCAAGTGATCCCCCTGGACAAAGGATT
AGCTGCGAGTGTGTCCCTGGCTACAGCGGGAAGCTCTGTGAGACAGACAATGATGACTGTGTGGCCCAAGTG
CCGCCACGGGGCCAGTGCCTGGACACAATCAATGGCTACACATGCACCTGCCCCCAGGGCTTCAGTGGACCCCT
TCTGTGAACACCCCCACCCATGGTCCCTACTGCAGACCAGCCCATGCGACCAGTACGAGTGCCAGAACGGGGCC
CAGTGTCATCGTGGTGCAGCAGGAGCCACCTGCCGCTGCCACCAGGCTTCGCCGGCCCCAGATGCGAGAAGCT
CATCACTGTCAACTTCGTGGGCAAAGACTCCTACGTGGAAGTGGCCTCCGCCAAGGTCCGACCCCAAGGCCAACA
TCTCCCTGCAGGTGGCCACTGACAAGGACAACGGCATCCTTCTCTACAAAGGAGACAATGACCCCTGGCACTG
GAGCTGTACCAGGGCCACGTGCGGCTGGTCTATGACAGCCTGAGTTCCCTCCAACCACAGTGTACAGTGTGGA
GACAGTGAATGATGGGCAGTTTCACAGTGTGGAGCTGGTGACGCTAAACCAGACCCTGAACCTAGTAGTGGACA
AAGGAATCCAAAGAGCCTGGGGAAGCTCCAGAAGCAGCCAGCAGTGGGCATCAACAGCCCCCTCTACCTTGGA
GGCATCCCCACCTCCACCGGCCTCTCCGCCTTGCGCCAGGGCACGGACCGGCCTCTAGGCGGCTTCACGGATG
CATCCATGAGGTGCGCATCAACAACGAGCTGCAGGACTTCAAGGCCCTCCACCACAGTCCCTGGGGGTGTCAC
CAGGCTGCAAGTCCTGCACCGTGTGCAAGCACGGCCTGTGCCGCTCCGTGGAGAAGGACAGCGTGGTGTGCGAG
TGCCGCCCAGGCTGGACCGGCCCACTCTGCGACCAGGAGGCCCGGGACCCCTGCCTCGGCCACAGATGCCACCA
TGGAATAATGTGTGGCAACTGGGACCTCATACATGTGCAAGTGTGCCGAGGGCTATGGAGGGGACTTGTGTGACA
ACAAGAATGACTCTGCCAATGCCCTGCTCAGCCTTCAAGTGTACCATGGGCAGTGCCACATCTCAGACCAAGGG
GAGCCCTACTGCCTGTGCCAGCCCGGCTTTAGCGGCGAGCACTGCCAACAAGAGAATCCGTGCCTGGGACAAGT
AGTCCGAGAGGTGATCCGCCGCCAGAAAGGTTATGCATCATGTGCCACAGCCTCCAAGGTGCCCATCATGGAAT
GTCGTGGGGGCTGTGGGCCCCAGTGTGCCAGCCACCCGAGCAAGCGGCGGAAATACGTCTTCCAGTGCACG
GACGGCTCCTCGTTTGTAGAAGAGGTGGAGAGACACTTAGAGTGCGGCTGCCTCGCGTGTTCCTAAGCCCCCTGC
CCGCTGCTGCCACCTCTCGGACTCCAGCTTGATGGAGTTGGGACAGCCATGTGGGACCCCTGGTGATTTCAG
CATGAAGGAAATGAAGCTGGAGAGGAAGGTAAAGAAGAAGAGAATATTAAGTATATTTGTAAATAAACAACAAAAA
TAGAACTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 24A

MAPGWAGVGAAVRARLALALALASVLSGPPAVACPTKCTCSAASVDCHGLGLRAVPRGIPR
NAERLDLDRNNITRITKMDFAGLKNLRVLHLEDNQVSVIERGAFQDLKQLERLRLNKNKLQ
VLPELLFQSTPKLTRLDLSENQIQGIPRKAFRGITDVKNLQLDNNHISCIEDGAFRALRDL
EILTLLNNNNISRILVTSFNHMPKIRTLRLHSNHLYCDCHLAWLSDWLRQRRTVGQFTLCMA
PVHLRGFNVADVQKKEYVCPAPHSEPPSCNANSISCPSPCTCSNNIVDCRGKGLMEIPANL
PEGIVEIRLEQNSIKAIPAGAFTQYKKLKRIDISKNOISDIAPDAFQGLKSLTSLVLYGNK
ITEIAKGLFDGLVSLQLLLLLNANKINCLRVNTFQDLQNLNLLSLYDNKLQOTISKGLFAPLO
SIQTLHLAQNPFFVCDCHLKWLADYLDNPIETSGARCSSPRRLANKRISQIKSKKFRCSGS
EDYRSRFSSECFMDLVCPEKCRCEGTIVDCSNQKLVRIPSHLPEYVTDLRLNDNEVSVLEA
TGIFKKLPNLRKINLSNNKIKEVREGAFDGAASVQELMLTGNQLETVHGRVFRGLSGLKTL
MLRSNLISCVSNDTFAGLSSVRLLSLYDNRITTTITPGAFTTLVSLSTINLLSNPFNCNCHL
AWLGKWLRRKRIVSGNPRCQKPFFLKEIPIQDVAIQDFTCDGNEESSCQLSPRCPEQCTCM
ETVVRCSNKGRLALPRGMPKDVTELYLEGNHILTAVPRELSALRHLLTLIDLSNNSISMLTNY
TFSNMSHLSTLILSYNRLRCIPVHAFNGLRSLRVLTTLHGNDISSVPEGSFNDLTSLSHLAL
GTNPLHCDCSLRWLSEWVKAGYKEPGIARCSSPEPMADRLLLTTPTHRFOCKGPVDINIVA
KCNACLSSPCKNNGTCTQDPVELYRCACPYSYKGKDCTVPINTCIQNPCQHGGTCHLSDSH
KDGFS CSCPLGFEGQRCEINPDDCEDNDCENNATCVDGINNYVCICPPNYTGELCDEVIDH
CVPENLNCQHEAKCIPLDKGFSCECVPGYSGKLCETDNDDCVAHKCRHGAQCVDTINGYTC
TCPQGFSGPFCEHPPPMVLLQTSPCDQYECQNGAQCIVVQQEPTCRCPPGFAGPRCEKLIT
VNFVGKDSYVELASAKVRPQANISLQVATDKDNGILLYKGDNDPLALELYQGHVRLVYDSL
SSPPTTVYSVETVNDGQFHSVELVTNLNQLNLVVDKGTPKSLGKLQKQPAVGINSPLYLGG
IPTSTGLSALRQGTDRPLGGFHGCIHEVRINNELQDFKALPPQSLGVSPGCKSCTVCKHGL
CRSVEKDSVVCECRPGWTGPLCDQEARDPCLGHRCHHGKCVATGTSYMCKCAEGYGGDLCD
NKNDSANACSAFKCHHGQCHISDQGEPYCLCQPGFSGEHCQQENPCLGQVVREVIRRQKGY
ASCATASKVPIMECRGGCGPQCCQPTRSKRRKYVFQCTDGSSFVEEVERHLECGCLACS

FIGURE 24B

Signal peptide:

amino acids 1-27

Important features of the protein:

Signal peptide:

Amino acids 1-25

Transmembrane domain:

Amino acids 169-192

N-glycosylation sites:

Amino acids 105-109;214-218;319-323;350-354;368-372;379-383

cAMP- and cGMP-dependent protein kinase phosphorylation sites:

Amino acids 200-204;238-242

Tyrosine kinase phosphorylation site:

Amino acids 207-214

N-myristoylation sites:

Amino acids 55-61;215-221;270-276

Prokaryotic membrane lipoprotein lipid attachment site:

Amino acids 259-270

TNFR/NGFR family cysteine-rich region proteins:

Amino acids 89-96

FIGURE 25

CAGTTTCTTCATCTGTAAACATCAAATGAATAATAATACCAATCTCCTAGACTTCATAAGA
GGATTAAACAAAGACAAAATATGGGAAAAACATAACATGGCGTCCCATAAATTATTAGATCT
TATTATTGACACTAAAATGGCATTAAAAATTACCAAAGGAAGACAGCATCTGTTTCTCTCT
TTGGTCCTGAGCTGGTTAAAAGGAACACTGGTTGCCCTGAACAGTCACACTTGCAACCATG
ATGCCTAAACATTGCTTTCTAGGCTTCCTCATCAGTTTCTTCTTACTGGTGTAGCAGGA
ACTCAGTCAACGCATGAGTCTCTGAAGCCTCAGAGGGTACAATTTTCAGTCCCGAAATTTT
CACAACATTTTGCAATGGCAGCCTGGGAGGGCACTTACTGGCAACAGCAGTGTCTATTTT
GTGCAGTACAAAATCATGTTCTCATGCAGCATGAAAAGCTCTCACCAGAAGCCAAGTGGA
TGCTGGCAGCACATTTCTTGTAACCTCCCAGGCTGCAGAACATTGGCTAAATATGGACAG
AGACAATGGAAAAATAAAGAAGACTGTTGGGGTACTCAAGAACTCTCTTGACCTTACC
AGTGAAACCTCAGACATACAGGAACCTTATTACGGGAGGGTGAGGGCGGCCTCGGCTGGG
AGCTACTCAGAATGGAGCATGACGCCGCGGTTCACTCCCTGGTGGGAAACAAAAATAGAT
CCTCCAGTCATGAATATAACCCAAGTCAATGGCTCTTTGTTGGTAATTCTCCATGCTCCA
AATTTACCATATAGATACCAAAGGAAAAAAATGTATCTATAGAAGATTACTATGAACTA
CTATACCGAGTTTTTTATAATTAACAATTCACTAGAAAAGGAGCAAAAGGTTTATGAAGGG
GCTCACAGAGCGGTTGAAATTGAAGCTCTAACACCACACTCCAGCTACTGTGTAGTGGCT
GAAATATATCAGCCCATGTTAGACAGAAGAAGTCAGAGAAGTGAAGAGAGATGTGTGGAA
ATTCCATGACTGTGGAATTTGGCATTGAGCAATGTGGAAATTCTAAAGCTCCCTGAGAA
CAGGATGACTCGTGTTTGAAGGATCTTATTTAAAATTGTTTTTTGTATTTTCTTAAAGCAA
TATTCAGTGTACACCTTGGGGACTTCTTTGTTTATCCATTCTTTTATCCTTTATATTTT
ATTTGTAACTATATTTGAACGACATTCCCCCGAAAAATTGAAATGTAAAGATGAGGCA
GAGAATAAAGTGTTCTATGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 26

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA145887
><subunit 1 of 1, 262 aa, 1 stop
><MW: 30419, pI: 8.44, NX(S/T): 5
MPKHCFLGFLISFFLTGVAGTQSTHESLKPQRVQFQSRNFHNIQWQPGRALTGNSSVYF
VQYKIMFSCSMKSSHQKPSGCWQHISCNFPGCRTLAKYGQRQWKNKEDCWGTQELSCDLT
SETSDIQEPYYGRVRAASAGSYSEWSMTPRFTPWWETKIDPPVMNITQVNGSLLVILHAP
NLPYRYQKEKNVSIEDYYELLYRVFIINNSLEKEQKVYEGAHRAVEIEALTPHSSYCVVA
EIIYQPMIDRRSQRSEERCVEIP
```

Important features of the protein:**Signal peptide:**

Amino Acids 1-20

N-glycosylation sites:

Amino acids 55-59;165-169;170-174;191-195;208-212

N-myristoylation sites:

Amino acids 17-23;20-26;220-226

GGAAGGGGAGGAGCAGGCCACACAGGCCACAGGCCGGGTGAGGGACCTGCCAGACCTGGAGGGTCTCGCTCTGTCT
 ACACAGGCTGGAGTGCAGTGGTGTGATCTTGGCTCATCGTAACCTCCACCTCCCGGGTTCAGTGATTCTCATG
 CCTCAGCCTCCCGAGTAGCTGGGATTACAGGTGGTGA CTTC AAGAGTGACTCCGTCGGAGGAAAATGACTCCC
 CAGTTCGCTGCTGCAGACGACACTGTTCTCTGTAGTCTGCTCTTCTGGTGCCCAAGGTGCCACGGCAGGGGCCA
 CAGGGAAGACTTTCTGTTCTGCAGCCAGCGAAGCCAGACACACAGGAGCAGCTCCACTACAACCCACACCAG
 ACCTGCGCATCTTCCCTCAGAACTCCGAAGAGGCCCTCACAGTCCATGCCCCCTTCCCTGCAGCCACCCTGCT
 TCCCGATCCTTCCCTGACCCCAGGGGCTCTACCACTTCTGCCTCTACTGGAACCGACATGCTGGGAGATTACA
 TCTTCTCTATGGCAAGCGTGACTTCTTGCTGAGTGACAAAGCCTCTAGCCTCCTCTGCTTCCAGCACCCAGGAGG
 AGAGCCTGGCTCAGGGCCCCCGCTGTTAGCCACTTCTGTCACTCCTGGTGGAGCCCTCAGAACATCAGCCCTG
 CCCAGTGCCGCCAGCTTTCACCTTCTCCTTCCACAGTCTCTCCCAACCGGCCCTCACAATGCCCTCGGTGGACAT
 GTGCGAGCTCAAAAGGGACCTCAGTGTCTCAGCCAGTTCTCTGAAGCATCCCGAAGCCTCAAGGAGGCCCT
 CGGCTGCCCCCGCCAGCCAGCAGATCTGCAGAGCCCTGGAGTGCAAACTGACCTCTGTGAGATTCTATGGGGGACATG
 GTGTCTTTCGAGGAGGACCGGATCAACGCCACGGTGTGGAAGCTCCAGCCCACAGCCGGCCCTCCAGGACCTGCA
 CATCCACTCCCGGCAGGAGGAGGAGCAGAGCGAGATCATGGAGTACTCGGTGCTGCTGCCCTCGAACACTCTTCC
 AGAGGACGAAAGGCCCGGAGCGGGGAGGCTGAGAAGAGACTCTCTGGTGGACTTCAGCAGCCAGGCCCTGTTCT
 CAGGACAAAGAATTCAGCCAACTCTGGTGGAGAGTCTTGGGAGTTGGTATGAGACAGAACCAAGTAGCCAA
 CCTCAGGAGCCCGTGGTGCTCACTTCCAGCACCAGCTACAGCCGAAGAATGTGACTCTGCAATGTGTGTTCT
 GGGTTGAAGACCCCACTTGTAGCAGCCCGGGGCATTTGGAGCAGTGTGGGTGTGAGACCGTCAGGAGAGAAACC
 CAAACATCCTGCTTCTGCAACCACTTGACCTACTTTGCAGTGCTGATGGTCTCCTCGGTGGAGGTGGACGCCGT
 GCACAAGCACTACCTGAGCCTCCTCTCCTACGTGGGCTGTGTGCTCTCTGCCCTGGCCTGCCTTGTCAACATTG
 CCGCTACCTCTGCTCCAGGGTGCCCCTGCCGTGCAGGAGGAACCTCGGGACTACACCATCAAGGTGCACATG
 AACCTGCTGTGGCCGTCTTCTGCTGGACAGCAGCTTCTGCTCAGCGAGCCGGTGGCCCTGACAGGCTCTGA
 GGCTGGCTGCCGAGCCAGTGCCATCTTCTGCATTTCTCCTGCTCACTGCTCTTCTGGATGGGCCTCGAGG
 GGTACAACCTCTACCGACTCGTGGTGGAGGTCTTTGGCACCTATGTCCCTGGCTACCTACTCAAGCTGAGCGCC
 ATGGGCTGGGGCTTCCCATCTTTCTGGTGACGCTGGTGGCCCTGGTGGATGTGGACAACTATGGCCCATCAT
 CTTGGCTGTGCATAGGACTCCAGAGGGCGTCATCTACCTTCCATGTGCTGGATCCGGGACTCCCTGGTTCAGT
 ACATACCAACCTGGGCCTCTTCAGCCTGGTGTCTTCTGTTCAACATGGCCATGCTAGCCACCATGGTGGTGAG
 ATCCTGCGGCTGCGCCCCACACCCAAAGTGGTGCATGTGCTGACACTGTGGCCCTCAGCCTGGTCTTGG
 CCTGCCCTGGGCCTTGATCTTCTTCTCCTTTGCTTCTGGCACCTTCCAGCTTGTGCTCCTCTACCTTTTTCAGCA
 TCATCACCTCCTTCCAAGGCTTCTTCATCTTTCATCTGGTACTGGTCCATGCGGCTGCAGGCCCGGGGTGGCCCC
 TCCCTCTGAAGAGCAACTCAGACAGCGCCAGGCTCCCATCAGCTCGGGCAGCACCTCGTCCAGCCGCATCTA
 GGCCCTCCAGCCACCTGCCCATGTGATGAAGCAGAGATGCGGCCCTCGTCGCACACTGCCTGTGGCCCCCGAGCC
 AGGCCAGCCCCAGGCCAGTTCAGCCGCAGACTTTGGAAGCCCAACGACCATGGAGAGATGGGCCGTGGCCATG
 GTGACCGAATCCCGGGCTGGGCTTTTGTAATGGCTTGGGACACTCGGCTCTCACTCAGCTCCCACGGGAC
 TCAGAAGTGCGCCGCCATGTGCTGCCTAGGGTACTGTCCCCACATCTGTCCCAACCCAGCTGGAGGCCCTGGTCTCT
 CTTTACAACCCCTGGGCCAGCCCTCATTTGCTGGGGGCCAGGCCTTGGATCTTGAGGGTCTGGCACATCCTTAA
 TCCTGTGCCCTGCCTGGGACAGAAATGTGGCTCCAGTTGCTCTGTCTCTCGTGGTCAACCTGAGGGCACTCTG
 CATCCTCTGTCACTTTTAACTTCAGGTGGCACCAGGGCGAATGGGGCCAGGGCAGACCTTCAGGGCCAGAGCC
 CTGGCGGAGGAGAGGCCCTTTGCGCAGGACACAGCAGCAGCTCGCCTACTCTGAGCCCAAGCCCCCTCCTCTC
 CTAGCCCCCAGTCTCCTCCCATCTTCCCTGGGGTCTCTCCTCTCCAGGCCCTCCTTGTCTCCTTCGTTT
 ACAGCTGGGGGTCCCCGATTCCAATGCTGTTTTTTGGGGAGTGGTTTCCAGGAGCTGCCTGGTGTCTGCTGTAA
 ATGTTTTGTCTACTGCACAAGCCTCGGCCCTGCCCTGAGCCAGGCTCGGTACCGATGCGTGGGCTGGGCTAGGTC
 CCTCTGTCCATCTGGGCCTTTGTATGAGCTGCATTGCCCTTGCTCACCTGACCAAGCACACGCCTCAGAGGGG
 CCTCAGCCTCTCCTGAAGCCCTCTTGTGGCAAGAAGCTGGGACCATGCCAGTCCCCTGTGGTTTCCATCCCAC
 CACTCCAAGGACTAGACTGACCTCCTCTGGTGACACTGGCTAGAGCTGACCTCTCTCAAGAGTTCTCTC
 CAAGCCCCCAAATAGACTCCAGCGCCCTCGGCCCCCATCATGGTTAATTCTGTCTCAACAAACACACACGGGTA
 GATTGCTGGCCTGTTGTAGGTGGTAGGGACACAGATGACCGACCTGGTCACTCTCCTGCCAACATTTCAGTCTG
 GTATGTGAGGCGTGCCTGAAGCAAGAACTCCTGGAGCTACAGGGACAGGGAGCCATCATTCCTGCCTGGGAATC
 CTGGAAGACTTCTCTGAGGAGTCAGCGTTCAATCTTGACCTTGAAGATGGGAAGGATGTTCTTTTACGTACCA
 ATTCTTTTGTCTTTTGATATTAAGAAAGATACATGTTCAATTGTAGAGAATTTGGAACCTGTAGAAGAGAATCA
 AGAAGAAAAATAAAATCAGCTGTTGTAATCGCCTAGCAAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA
 AAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA

FIGURE 28

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50921

<subunit 1 of 1, 693 aa, 1 stop

<MW: 77738, pI: 8.87, NX(S/T): 7

MTPQSLLQTTLFLLSLLFLVQGAHGRGHREDFRFC SQRNQTHRSSLHYKPTPDLRISIENS
EEALT VHAPFPAAHPASRSFPDPRGLYHFC LYWNRHAGRLHLLY GKRD FLLSDKASSLLCF
QHQEESLAQGPPLLATSVTSWWSPQNISLPSAASF TFSFHSPHTAAHNASVDMCELKRDL
QLLSQFLKHPQKASRRPSAAPASQQQLQSLESKLTSVRFMGDMV SFEE DRINATVWKLQPTA
GLQDLHIHSRQEEEQSEIMEYSVLLPRTL FQRTKGRSGEAEKRLLL VDFSSQALFQDKNSS
QVLGEKVLGIVVQNTKVANLTEPVVLT FQHQLQPKNVT LQCVFWVEDPTLSSPGHWSSAGC
ETVRRETQTSCFCNHLTYFAVLMVSSVEVD AVHKHYLSLLSYVGCVV SALACLVTIAAYLC
SRVPLPCR RKPRDYTIKVH MNLLLAVFLLDTSFLLSEPVALTGSEAGCRASAI FLHFSLLT
CLSWMGLEGYNLYRLVVEVFGTYVPGYLLKLSAMGWGFPI FLVTLVALVDVDNYGP IILAV
HRTPEGVIYPSMCWIRDSLVS YITNLGLFSLVFLFN MAMLATMVVQILRLRPHTQKWSHVL
TLLGLSLVLGLPWALIFFSFASGTFQLVVL YLFSIITSFQGF LIFIWYWSMRLQARGGPSP
LKSNSDSARLPISSGSTSSSRI

Important features:**Signal peptide:**

amino acids 1-25

Putative transmembrane domains:

amino acids 382-398, 402-420, 445-468, 473-491, 519-537, 568-590
and 634-657

Microbodies C-terminal targeting signal.

amino acids 691-693

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 198-201 and 370-373

N-glycosylation sites.

amino acids 39-42, 148-151, 171-174, 234-237, 303-306, 324-327
and 341-344

G-protein coupled receptors family 2 proteins

amino acids 475-504

FIGURE 29A

TGTGCAGAATTGTACAGTTGCGAAACCATGTCGCTGGCAGCTGGTGCTGGCGGTGGAGAC
TTCCCTGTGCGGTGCTCAGTGCATCTGCACCCGTGGGGGAGGGAGCTCTTTCTCTGGCCC
TGCAGTCACCTGAGGTTGTTACCATTATGAACGGCCGCTGGGACCCCCGCATGTGCATGT
ACTCCCCCAGAGTGTCCGGGGGCCCCAGCCAAGGGACACATCTCACGCAGCTGGGAACAT
GTGCAGGCTGATGAAGAGAACCGGATGAGGGCTTCACATGAGGAAGCATGTGGCCAGGTC
CTCTCAGAACATCAGCCTCATCTTCCTGTCTCTGATCTATTTACCAACCACCCCATGTG
TCTCTAGAACCCCACTGTAGCGAGCTGGAGAGAGGACTGTCCTGAGGGCAGCAGGCCTGG
TTGCAGCTGGCGTGGGGGTCTCAGAATGGAGCCCTCAGCCCTGAGGAAAAGCTGGCTCGGA
GCAGGAGGAGGGCTTTGAGGGGCTGCCAGAAGGGTCACTGACCTGGGGATGGTCTCCAA
TCTCCGGCGCAGCAACAGCAGCCTCTTCAAGAGCTGGAGGCTACAGTGCCCTTCGGCAA
CAATGACAAGCAAGAAAGCCTCAGTTTCGTGGATTCTGAAAACATCAAGAAGAAAGAATG
CGTGTATTTTGTGGAAAGTTCCAAACTGTCTGATGCTGGGAAGGTGGTGTGTGTCAGTGTGG
CTACACGCATGAGCAGCACTTGGAGGAGGCTACCAAGCCCCACACCTTCAGGGCACACA
GTGGGACCCAAAGAAACATGTCCAGGAGATGCCAACCGATGCCTTTGGCGACATCGTCTT
CACGGGCCTGAGCCAGAAGGTGAAAAAGTACGTCCGAGTCTCCCAGGACACGCCCTCCAG
CGTGATCTACCACCTCATGACCCAGCACTGGGGGCTGGACGTCCCCAATCTCTTGATCTC
GGTGACCGGGGGGGCCAAAGAACTTCAACATGAAGCCGCGGCTGAAGAGCATTTTCCGCAG
AGGCCTGGTCAAGGTGGCTCAGACCACAGGGGCTGGATCATCACAGGGGGGTCCCACAC
CGGCGTCATGAAGCAGGTAGGCGAGGCGGTGCGGGACTTCAGCCTGAGCAGCAGCTACAA
GGAAGGCGAGCTCATCACCATCGGAGTCGCCACCTGGGGCACTGTCCACCGCCGCGAGGG
CCTGATCCATCCCACGGGCAGCTTCCCCGCCGAGTACATACTGGATGAGGATGGCCAAGG
GAACCTGACCTGCCTAGACAGCAACCACTCTCACTTCATCCTCGTGACGACGGGACCCA
CGGCCAGTACGGGGTGGAGATTCTCTGAGGACCAGGCTGGAGAAGTTCATATCGGAGCA
GACCAAGGAAAGAGGAGGTGTGGCCATCAAGATCCCCATCGTGTGCGTGGTGCTGGAGGG
CGGCCCCGGGCACGTTGCACACCATCGACAACGCCACCACCAACGGCACCCCTGTGTGGT
TGTGGAGGGCTCGGGCCGCGTGGCCGACGTCATTGCCAGGTGGCCAACCTGCCTGTCTC
GGACATCACTATCTCCCTGATCCAGCAGAACTGAGCGTGTTCCTCCAGGAGATGTTTGA
GACCTTCACGGAAGCAGGATTGTGCGAGTGGACCAAAAAGATCCAAGATATTGTCCGGAG
GCGGCAGCTGCTGACTGTCTTCCGGGAAGGCAAGGATGGTCAGCAGGACGTGGATGTGGC
CATCTTGCAGGCCTTGCTGAAAGCCTCACGGAGCCAAGACCACTTTGGCCACGAGAACTG
GGACCACCAGCTGAAACTGGCAGTGGCATGGAATCGCGTGGACATTGCCCGCAGTGAGAT
CTTCATGGATGAGTGGCAGTGGAAAGCCTTCAGATCTGCACCCACGATGACAGCTGCACCT
CATCTCCAACAAGCCTGAGTTTGTGAAGCTCTTCCTGGAAAACGGGGTGCAGCTGAAGGA
GTTTGTACCTGGGACACCTTGCTCTACCTGTACGAGAACCTGGACCCCTCCTGCCTGTT
CCACAGCAAGCTGCAAAAGGTGCTGGTGGAGGATCCCGAGCGCCCGCTTGCGCGCCCGC
GGCGCCCCGCTGCAGATGCACCACGTGGCCAGGTGCTGCGGGAGCTGCTGGGGGACTT

FIGURE 29B

CACGCAGCCGCTTTATCCCCGGCCCCGGCACAACGACCGGCTGCGGCTCCTGCTGCCCCGT
TCCCCACGTCAAGCTCAACGTGCAGGGAGTGAGCCTCCGGTCCCTCTACAAGCGTTCCTC
AGGCCATGTGACCTTCACCATGGACCCCATCCGTGACCTTCTCATTTGGGCCATTGTCCA
GAACCGTCGGGAGCTGGCAGGAATCATCTGGGCTCAGAGCCAGGACTGCATCGCAGCGGC
CTTGGCCTGCAGCAAGATCCTGAAGGAAGTGTCCAAGGAGGAGGAGGACACGGACAGCTC
GGAGGAGATGCTGGCGCTGGCGGAGGAGTATGAGCACAGAGCCATCGGGGTCTTCACCGA
GTGCTACCGGAAGGACGAAGAGAGAGGCCAGAACTGCTCACCCGCGTGTCCGAGGCCTG
GGGGAAGACCCACCTGCCTGCAGCTCGCCCTGGAGGCCAAGGACATGAAGTTTGTGTCTCA
CGGGGGCATCCAGGCCTTCCTGACCAAGGTGTGGTGGGGCCAGCTCTCCGTGGACAATGG
GCTGTGGCGTGTGACCTGTGCATGCTGGCCTTCCCGCTGCTCCTCACCGGCCTCATCTC
CTTCAGGGAGAAGAGGCTGCAGGATGTGGGCACCCCCGCGCCCGCGCCCGTGCCTTCTT
CACCGCACCCGTGGTGGTCTTCCACCTGAACATCCTCTCCTACTTCGCCTTCCTCTGCCT
GTTTCGCCTACGTGCTCATGGTGGACTTCCAGCCTGTGCCCTCCTGGTGCAGTGTGCCAT
CTACCTCTGGCTCTTCTCCTTGGTGTGCGAGGAGATGCGGCAGCTCTTCTATGACCCTGA
CGAGTGCGGGCTGATGAAGAAGGCAGCCTTGTACTTCAGTGACTTCTGGAATAAGCTGGA
CGTCGGCGCAATCTTGCTCTTCGTGGCAGGGCTGACCTGCAGGCTCATCCCGGCGACGCT
GTACCCCGGGCGCGTCATCCTCTCTCTGGAAGTTCATCCTGTTCTGCCTCCGGCTCATGCA
CATTTTACCATCAGTAAGACGCTGGGGCCCAAGATCATCATTGTGAAGCGGATGATGAA
GGACGTCTTCTTCTTCTCTCTCTGCTGGCTGTGTGGGTGGTGTCTTTCGGGGTGGCCAA
GCAGGCCATCCTCATCCACAACGAGCGCCGGGTGGACTGGCTGTTCCGAGGGGCCGTCTA
CCACTCCTACCTCACCATCTTCGGGCAGATCCCGGGCTACATCGACGGTGTGAACTTCAA
CCCGGAGCACTGCAGCCCCAATGGCACCGACCCCTACAAGCCTAAGTGCCCCGAGAGCGA
CGCGACGCAGCAGAGGCCGGCCTTCCCTGAGTGGCTGACGGTCCTCCTACTCTGCCTCTA
CCTGCTCTTCACCAACATCCTGCTGCTCAACCTCCTCATCGCCATGTTCAACTACACCTT
CCAGCAGGTGCAGGAGCACACGGACCAGATTTGGAAGTTCAGCGCCATGACCTGATCGA
GGAGTACCACGGCCGCCCGCGCGCGCCCGCCCTTCATCCTCCTCAGCCACCTGCAGCT
CTTCATCAAGAGGGTGGTCTGAAGACTCCGGCCAAGAGGCACAAGCAGCTCAAGAACAA
GCTGGAGAAGAAGCAGGAGGCGGCCCTGCTATCCTGGGAGATCTACCTGAAGGAGAACTA
CCTCCAGAACCGACAGTTCCAGCAAAAGCAGCGGCCCGAGCAGAAGATCGAGGACATCAG
CAATAAGGTGACGCCATGGTGGACCTGCTGGACCTGGACCCACTGAAGAGGTTCGGGCTC
CATGGAGCAGAGGTGGCCTCCCTGGAGGAGCAGGTGGCCAGACAGCCCGAGCCCTGCA
CTGGATCGTGAGGACGCTGCGGGCCAGCGGCTTCAGCTCGGAGGCGGACGTCCCCACTCT
GGCCTCCAGAAGGCCGCGGAGGAGCCGGATGCTGAGCCGGGAGGCAGGAAGAAGACGGA
GGAGCCGGGCGACAGCTACCACGTGAATGCCCGGCACCTCCTTACCCCAACTGCCCTGT
CACGCGCTTCCCCGTGCCCAACGAGAAGGTGCCCTGGGAGACGGAGTTCCTGATCTATGA

FIGURE 29C

CCCACCC'TTTTACACGGCAGAGAGGAAGGACGCGGCCGCCATGGACCCCATGGGAGACAC
CCTGGAGCCACTGTCCACGATCCAGTACAACGTGGTGGATGGCCTGAGGGACCGCCGGAG
CTTCCACGGGCCGTACACAGTGCAGGCCGGGTTGCCCTGAACCCCATGGGCCGCACAGG
ACTGCGTGGGCGCGGGAGCCTCAGCTGCTTCGGACCCAACCACACGCTGTACCCCATGGT
CACGCGTGGAGGCGGAACGAGGATGGAGCCATCTGCAGGAAGAGCATAAAGAAGATGCT
GGAAGTGC'TGGTGGTGAAGCTCCCTCTCTCCGAGCAC'TGGGCCCTGCCTGGGGGCTCCCG
GGAGCCAGGGGAGATGCTACCTCGGAAGCTGAAGCGGATCCTCCGGCAGGAGCACTGGCC
GTCTTTTGA AA ACTTGCTGAAGTGC GGCATGGAGGTGTACAAAGGCTACATGGATGACCC
GAGGAACACGGACAATGCCTGGATCGAGACGGTGGCCGTCAGCGTCCACTTCCAGGACCA
GAATGACGTGGAGCTGAACAGGCTGAACTCTAACCTGCACGCCTGCGACTCGGGGGCCTC
CATCCGATGGCAGGTGGTGGACAGGCGCATCCCACTCTATGCGAACCACAAGACCCCTCCT
CCAGAAGGCAGCCGCTGAGTTCGGGGCTCACTAC TGACTGTGCCCTCAGGCTGGGCGGCT
CCAGTCCATAGACGTTCCCCCAGAAACCAGGGCTTCTCTCTCCTGAGCCTGGCCAGGAC
TCAGGCTGTTCCTGGGCCCTGCACATGATGGGGTTTGGTGGACCCAGTGCCCCCTCACGGC
TGCCGCAAGTCTGCTGCAGATGACCTCATGAACTGGAAGGGGTCAAGGTGACCCGGGAGG
AGAGCTCAAGACAGGGCACAGGCTACTCAGAGCTGAGGGGCCCCTGGGACCCTTGGCCAT
CAGGCGAGGGGCTGGGCCTGTGCAGCTGGGCCCTTGGCCAGAGTCCACTCCCTTCTCTGGC
TGTGTCAACCCGAGCAGCTCATCCACCATGGAGGTCAATTGGCCTGAGGCAAGTTCCCCGG
AGAGTCGGGATCCCTGTGGCCCCCTCAGGCCATGTCTGTGAGGAAGGGGCCCTGCCAC
TCTCCCCAAGAGGGCCTCCATGTTTCGAGGTGCCTCAACATGGAGCCTTGCCCTGGCCTGG
GCTAGGGGCACTGTCTGAACTCCTGACTGTCAGGATAAACTCCGTGGGGGTACAGGAGCC
CAGACAAAGCCCAGGCCTGTCAAGAGACGCAGAGGGCCCCCTGCCAGGGTTGGCCCCAGGG
ACCC'TGGGACGAGGCTGCAGAAGCTCTCCCTCCCTACTCCCTGGGAGCCACGTGCTGGCC
ATGTGGCCAGGGACGGCATGAGCAGGAGGCGGGGACGTGGGGGCCTTCTGGTTTGGTGTC
AACAGCTCACAGGAGCGTGAACCATGAGGGCCCTCAGGAGGGGAACGTGGTAAAACCCAA
GACATTAAATCTGCCATCTCAGGCCTGGCTGGCTCTTCTGTGCTTTCCACAAATAAAGTT
CCTGACACGTCCAGGGCCAGGGGCTGTGTGACGGCTGCCTGAAGTTCTCCTCGATCCCC
GGTGAGCTTCTGACGCTGTGGATGTCTGACGCCCTCAGCCCTACCCCCAAGTTTCT
CCTCTGACCCATCAGCTCCCTGTCTTCATTTTCCTAAACCTGGGCTCCAGCATCGTCCCC
AAGCCCACCAGGCCAGGATGCAGGCATCCACATGCCCTCCTCCTTGGCTTCCCCTGCGTG
GTGGTGCCAATGTGCCCTGGCACCCCTGCAGAGGCTCCGGATGGAGCCTGGGGCTGCCTG
GCCACTGAGCACTGGCCGAGGTGATGCCACCCCTTCCCTGGACAGGCCTCTGTCTTCCAC
CTGACCCAAAGCTCTCTAGCCACCCCTTGTCCTCCAGTAT

FIGURE 30

><DNA226659 [min]
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA226659
><subunit 1 of 1, 1503 aa, 1 stop
><MW: 171226, pI: 7.73, NX(S/T): 8

MEPSALRKAGSEQEEGFEGLP RRVTDLGMVSNLRRSNSSLFKSWRLQCPFGNNDKQESLS
SWIPENIKKKECVYFVESSKLS DAGKVVCQCGYTHEQHLEEATKPHTFQGTQWDPKKHVQ
EMPTDAFGDIVFTGLSQVKVKYVRVSQDTPSSVIYHLMTQHWGLDVPNLLISVTGGAKNF
NMKPRLKSI FRRGLVKVAQTTGAWIITGGSHTGVMKQVGEAVRDFSLSSSYKEGELITIG
VATWGTVHRREGLIHPTGSFPAEYILDEDDGQGNLTCLDSNHSHFILVDDGTHGQYGV EIP
LRTRLEKFISEQTKERGGVAIKIPIVCVVLEGGPGTLHTIDNATTNGTPCVVVEGSGRVA
DVIAQVANLPVSDITISLIQOKLSVFFQEMFETFTESRIVEWTKKIQDIVRRRQLLTVFR
EGKDGQQDQVDVAILQALLKASRSQDHFGHENWDHQLKLAVAWNRVDIARSEIFMDEWQWK
PSDLHPTMTAALISNKPEFVKLFLENGVQLKEFTWDTLLYLYENLDPSCLFHSKLQKVL
VEDPERPACAPAAPRLQMHVVAQVLR ELLGDFTQPLYPRPRHNDRLRLLLVPVPHVKLNVO
GVSLRSLYKRSSGHVFTFTMDPIRDLLIWAIVQNRRELAGIIWAQSQDCIAALACSKILK
ELSKEEEDTDSSEMLALAE EYEHRAIGVFTECYRKDEERAQKLLTRVSEAWGKTTCLQL
ALEAKDMKFVSHGGIQAFLTKVWWGQLSVDNGLWRVTL CMLAFPLLLTGLISFREKRLQD
VGTPAARARAFFTAPVVVFHLNLSYFAFLCLFAYVLMVDFQPVPSWCECAIYLWLFSLV
CEEMRQLFYDPDECGLMKKAALYFSDFWNKLDVGAILLFVAGLTCRLIPATLYPGRVILS
LDFILFCLRLMHIFTISKTLGPKIIIVKRMMKDVFFFLFLLAVWVVSFGVAKQAILIHNE
RRVDWLFRGAVYHSYLTIFGQIPGYIDGVNFNPEHCSPNGTDPYKPKCPESDATQQRPAF
PEWLTVLLLCLYLLFTNILLNLLIAMFN YTFQQVQEHTDQIWKFORHDLIEEYHGRPAA
PPPFILLSHLQLFIKRVVLKTPAKRHKQLKNKLEKNEEAALLSWEIY LKENYLQNRQFQQ
KORPEQKIEDISNKVDAMVDLLDLDPLKRSGSMEQRLASLEEQVAQTARALHWIVRTLRA
SGFSSEADVPTLASQKAAE EPDAEPGGRKKTEEPGDSYHVNARHLLYPNCPVTRFPVPNE
KVPWETEFLIYDPPFYTAERKDAAAMPMDTLEPLSTIQYNVVDGLRDRRSFHGPYTVQ
AGLPLNPMGRTGLRGRGSLSCFGPNHTLYPMVTRWRNEDGAICRKS IKKMLEVLVVKLP
LSEHWALPGSREPGEMLPRLKLRILRQEHWP SFENLLKCGMEVYKGYMDDPRNTDNAWI
ETVAVSVHFQDQNDVELNRLNSNLHACDSGASIRWQVVDRIPLYANHKTLLQKAAAEFG
AHY

FIGURE 31

GATGGCGCAGCCACAGCTTCTGTGAGATTTCGATTTCTCCCCAGTTCCCCTGTGGGTCTGAGGGGACCAGAAGGG
TGAGCTACGTTGGCTTTCTGGAAGGGGAGGCTATATGCGTCAATTCCCCAAAACAAGTTTTGACATTTCCCCTG
AAATGTCATTCTCTATCTATTCACTGCAAGTGCCTGCTGTTCCAGGCCTTACCTGCTGGGCACTAACGGCGGAG
CCAGGATGGGGACAGAATAAAGGAGCCACGACCTGTGCCACCAACTCGCACTCAGACTCTGAACCTCAGACCTGA
AATCTTCTCTTCACGGGAGGCTTGGCAGTTTTTCTTACTCCTGTGGTCTCCAGATTTTCAGGCCTAAGATGAAAAG
CCTCTAGTCTTGCCTTCAGCCTTCTCTCTGCTGCGTTTTATCTCCTATGGACTCCTTCCACTGGACTGAAGACA
CTCAATTTGGGAAGCTGTGTGATCGCCACAAACCTTCAGGAAATACGAAATGGATTTTCTGAGATACGGGGCAG
TGTGCAAGCCAAAGATGGAAACATTGACATCAGAATCTTAAGGAGGACTGAGTCTTTGCAAGACACAAAGCCTG
CGAATCGATGCTGCCTCCTGCGCCATTTGCTAAGACTCTATCTGGACAGGGTATTTAAAAACTACCAGACCCCT
GACCATTTATACTCTCCGGAAGATCAGCAGCCTCGCCAATTCTTTCTTACCATCAAGAAGGACCTCCGGCTCTC
TCATGCCCACATGACATGCCATTGTGGGGAGGAAGCAATGAAGAAATACAGCCAGATTCTGAGTCACTTTGAAA
AGCTGGAACCTCAGGCAGCAGTTGTGAAGGC'TTTGGGGGAAGTAGACATTTCTTCTGCAATGGATGGAGGAGACA
GAAATAGGAGGAAAGTGATGCTGCTGCTAAGAATATTCGAGGTCAAGAGCTCCAGTCTTCAATACCTGCAGAGGA
GGCATGACCCCAAACCACCATCTCTTTACTGTACTAGTCTTGTGCTGGTCACAGTGTATCTTATTTATGCATTA
CTTGCTTCCTTGCATGATTGTCTTTATGCATCCCCAATCTTAATTGAGACCATACTTGTATAAGATTTTTGTAA
TATCTTTCTGCTATTGGATATATTTATTAGTTAATATATTTATTTATTTT'TTGCTATTTAATGTATTTATTTT
TTACTTGGACATGAACTTTAAAAAAATTCACAGATTATATTTATAACCTGACTAGAGCAGGTGATGTATTTTT
ATACAGTAAAAAAAAAAAAACCTTGTAATTC'TAGAAGAGTGGCTAGGGGGGT'TATTCATTTGTATTCAACTAAG
GACATATTTACTCATGCTGATGCTCTGTGAGATATTTGAAATTGAACCAATGACTACTTAGGATGGGTGTGGA
ATAAGTTTTTGATGTGGAATTGCACATCTACCTTACAATTACTGACCATCCCCAGTAGACTCCCCAGTCCCATAA
TTGTGTATCTTCAGCCAGGAATCCTACACGGCCAGCATGTATTTCTACAAATAAAGTTTTCTTTGCATACCAA
AAAAAAAAAAAAAAAAAAAA

FIGURE 32

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA83500

><subunit 1 of 1, 176 aa, 1 stop

><MW: 20056, pI: 9.13, NX(S/T): 0

MKASSLAFSLLSAAFYLLWTPSTGLKTLNLGSCVIATNLQEIRNGFSEIRGSVQAKDGNI
DIRILRRTESLQDTKPANRCCLLRHLLRLYLDRVFKNYQTPDHYTLRKISSLANSTLIK
KDLRLSHAHMTCHCGEAMKKYSQILSHFEKLEPQAAVVKALGELDILLQWMEETE